

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 18 Seconds

(without alignments)
1554.173 Million cell updates/sec

Title: US-09-424-705b-2

Perfect score: 1536

Sequence: 1 MKYLLPTAAAGLLLAQPA.....GSEQKLISEEDLNHHHHH 291

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857.5	55.8	268	2 A56446	Ig heavy chain V r
2	671	43.7	249	2 S41374	single chain Fv an
3	612	39.8	233	2 JCS322	p53 specific singl
4	545	35.5	144	2 B30502	Ig heavy chain V r
5	540.5	35.2	139	2 PS0024	Ig heavy chain pre
6	531	34.6	235	2 S25058	Ig kappa chain - m
7	527	34.3	287	4 PC4402	pelb leader/Ig hea
8	521.5	34.0	246	2 S38950	Ig gamma chain - m
9	521.5	34.0	246	2 S40295	Ig gamma-2a chain
10	519	33.8	107	2 A30562	Ig kappa chain V r
11	519	33.8	474	1 G2MS11	Ig gamma-2b chain
12	514	33.5	107	2 B30562	Ig kappa chain V r
13	514	33.5	130	1 JL0079	Ig kappa chain pre
14	513.5	33.4	120	2 S41394	Ig heavy chain V r
15	512.5	33.4	140	2 PH1482	Ig heavy chain V r
16	511.5	33.3	139	2 A27609	Ig heavy chain pre
17	508.5	33.1	140	1 HVMG7	Ig heavy chain pre
18	508.5	33.1	103	2 S29591	Ig kappa chain V r
19	506.5	33.0	120	2 B22769	Ig heavy chain V r
20	504	32.8	104	2 B49049	Ig kappa chain V r
21	503.5	32.8	122	2 S24287	Ig kappa chain V r
22	503.5	32.8	131	2 S66537	Ig heavy chain V r
23	503.5	32.8	139	1 MMS18	Ig heavy chain pre
24	501.5	32.6	469	2 S37483	Ig gamma-2a chain
25	501	32.6	106	2 PS0071	Ig kappa chain V r
26	501	32.6	120	2 S25175	Ig heavy chain V r
27	499.5	32.5	140	2 PH1489	Ig heavy chain V r
28	497.5	32.4	108	2 G30560	Ig kappa chain V r
29	497	32.4	118	2 S38565	Ig heavy chain V r

30	496	32.3	116	2 S55542	Ig heavy chain V r
31	496	32.3	121	2 A26405	Ig heavy chain V r
32	494.5	32.2	116	2 S53751	antibody Fab Jcl 1
33	494	32.2	107	2 S11118	Ig kappa chain V r
34	494	32.2	122	2 S20643	Ig heavy chain V r
35	493.5	32.1	140	2 PH1484	Ig heavy chain V r
36	493	32.1	107	2 PT0406	Ig kappa chain V r
37	492.5	32.1	151	2 PL0011	Ig kappa chain V r
38	492	32.0	123	2 E48677	Ig heavy chain V-D
39	491	32.0	107	2 PC4405	Ig kappa chain V r
40	491	32.0	107	2 S11119	Ig kappa chain V r
41	491	32.0	138	2 E32513	Ig heavy chain pre
42	490.5	31.9	123	2 S60067	Ig heavy chain V r
43	490.5	31.9	140	2 PH1488	Ig heavy chain V r
44	490	31.9	123	2 S20646	Ig heavy chain V r
45	489.5	31.9	140	2 PH1498	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (JH-3H scFv) - mouse (strain BALB/C)
C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_#revision 19-Jan-1996 #ext_change 16-Aug-1996
C/Accession: A56446
R/Tand, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident
A/Reference number: A56446; MUID:95229583; PMID:7713873
A/Accession: A56446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-268 <TAN>
A/Cross-references: GB:U20617
C/Keywords: heterotrimer; immunoglobulin

Query Match 55.8%; Score 857.5; DB 2; Length 268;
Best local similarity 65.3%; Pred. No. 1.4e-51;
Matches 175; Conservative 25; Mismatches 61; Indels 7; Gaps 3;

QY 21 MAQVQLQSGAEELIAPGASVKSCASGTFTRYYHWKORPGGLEWIGYINPARGYT 80
DB 1 MAQVQLQSGAEELVKKPGASVKLSCTTSFNIKDTYHWKORPEQGLEWIGRIAPANGIT 60
QY 81 NYNQKPKDKATLTITDKSSSTAYWQLSLTSEDSAVYYCARYPDHYSLDYWGCTTLTVS 140
DB 61 KDPKFOGKATTAADTSNAYVQLSLTSEDTAVYYCASYLTRYE-NYWGQGTIVTVS 119
QY 141 SAKTPELSEGFSEARVIVLTQSPAIMSASPGKAVTMTCSASSSVSNWYQKSGTS 200
DB 120 SGGGGS--GGGDSGGGSDIELTQSPAIMSASLGEVYMTSCRASSSVNFTYVQKSDAS 177
QY 201 PKRWIDYTKLASGVPAHFRSGSGTSYSLTISGMAEDPAATYYCOQWSNPFTFGSGTK 260
DB 178 PKRWVYTHLPKGVPAHFRSGSGSGNSYSLTISMGEDPAATYYCOQFSSPFTFGSGTK 227
QY 261 LEINRADT---APTGSEQKLISEEDLN 284
DB 238 LEIKRSAHHHHHGAEEQLISEEDLN 265

RESULT 2

S41374
single chain Fv antibody - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_#revision 06-Jan-1995 #ext_change 06-Jan-1995
C/Accession: S41374
R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A/Description: Construction and functional characterization of a single chain Fv antibod
A/Reference number: S41374

A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 43.7%; Score 671; DB 2; Length 249;
Best Local Similarity 56.0%; Pred. No. 6.9e-39;
Matches 140; Conservative 29; Mismatches 77; Indels 8; Gaps 2;

Qy 23 QVQLQSGAEALRPGASVKMSCKASGYTFTYTHMVKQRPQGGLWIGYINPSRGYTN 82
Db 1 QVQLQSGAEALRPGASVKLSCTASGFNPKDDYIHVKQRPKEGLEWIAIPASGNVKY 60
Qy 83 NQKFKDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSA 142
Db 61 VRFQDKATITADTSNTAYLLSLTSDTAVYCARRDITLYSLGYWGQGTTVTVSSR 120
Qy 143 KTTPKLEGEFSEARVDIVLTQSPAIMASPGKVTMTCSASSV-----SYNMWYQOK 196
Db 121 GGS--GGGGGGGSDIELTQSPVVPVIGESVISCRSKSLSDYDGDYILFWFLOR 178
Qy 197 SGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYYCQOWSSNPFTFG 256
Db 179 PQSPQLLIYRMSNLASGVDPDRFSGSGSGTSFTLRISRVEADVGYYCMQHREYPLTFG 238
Qy 257 SGTKLEINRA 266
Db 239 AGTKLEKRA 248

RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 39.8%; Score 612; DB 2; Length 233;
Best Local Similarity 53.6%; Pred. No. 6.8e-35;
Matches 133; Conservative 26; Mismatches 63; Indels 26; Gaps 5;

Qy 27 QQSGAEALRPGASVKMSCKASGYTFTYTHMVKQRPQGGLWIGYINPSRGYTNQKF 86
Db 1 QESGAEALRPGASVKLSCTTSFTNINDYVYHVKRPEQGLEWIGRIDPENGADMTSSR 60
Qy 87 KDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSAKTTP 146
Db 61 GVKATMTADTSNTAYLQLSLTSDTAVYCYC-----NAGMDYWGQGTTVTVSSG--- 110
Qy 147 KLEGEFSEARV-----DIVLTQSPAIMASPGKVTMTCSASSV-----SYNMWYQO 195
Db 111 ----GGSGGGRASGGGSDIELTQSPASLVSLGQRATISCRASKSVSTSGSYMHWNOQ 166
Qy 196 KSGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYYCQOWSSNPFTFF 255
Db 167 KQGPRLLIYVSNLESGVPAHFRGSGSGSGTDFTLNIHPVEEDAATYYCQHIRLTREE 226
Qy 256 GSGTKLEI 263
Db 227 G-GTKLEI 233

RESULT 4

B30502

Ig heavy chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: B30502
R:Eliait, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: B30502

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-144 <EIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 545; DB 2; Length 144;
Best Local Similarity 65.5%; Pred. No. 1.5e-30;
Matches 108; Conservative 11; Mismatches 22; Indels 24; Gaps

Qy 23 QVQLQSGAEALRPGASVKMSCKASGYTFTYTHMVKQRPQGGLWIGYINPSRGYTN 82
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTITGYVMHWKQRPQGGLAWIGYINPYNDGTYK 60
Qy 83 NQKPKDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSA 142
Db 61 NEKFKGKATLTSDKSSSTAYTELSSLASDAAVYCAR-----GGFDYWGQGTTLT--- 111
Qy 143 KTTPKLEGEFSEARVDIVLTQSPAIMASPGKVTMTCSASSV 187
Db 112 -----VDILLTQSPALLSVSPGERVSPFCRASQSI 141

RESULT 5

PS0024

Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A:Reference number: PS0023; MUID:892332725; PMID:3149944
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against P₁omonas
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology <IMM>
F:20/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted

Query Match 35.2%; Score 540.5; DB 2; Length 139;
Best Local Similarity 84.3%; Pred. No. 2.9e-30;
Matches 102; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 22 AQVQLQSGAEALRPGASVKMSCKASGYTFTYTHMVKQRPQGGLWIGYINPSRGYTN 81
Db 19 SQVQLQSGAEALRPGASVKMSCKASGYTFTAYMHWKQRPQGGLWIGYINPTGYTE 78
Qy 82 YNQKPKDKATLTDDKSSSTAYMQLSLTSDSAVYCYAR-YYDDHYSLDYWGQGTTLTVS 140
Db 79 YNQKPKDKATLTADKSSSTAYMQLSLTSDSAVYCYCTSYNYEGAMDYWGQGTISVTS 138
Qy 141 S 141
Db 139 S 139

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 14 Seconds

(without alignments)
862.115 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1535
Sequence: 1 MRYLLPTAAAGLLLAOPA.....GSEQKLISEEDINSHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

T number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508.5	33.1	140	1 HV02_MOUSE	P01746 mus musculu
2	508	33.1	120	1 HV03_MOUSE	P01747 mus musculu
3	503.5	32.8	139	1 HV07_MOUSE	P01751 mus musculu
4	500	32.6	107	1 KV6F_MOUSE	P04940 mus musculu
5	497	32.4	107	1 KV6J_MOUSE	P04944 mus musculu
6	495	32.2	107	1 KV6I_MOUSE	P04943 mus musculu
7	494	32.2	107	1 KV6H_MOUSE	P04942 mus musculu
8	491	32.0	107	1 KV6G_MOUSE	P04941 mus musculu
9	482.5	31.4	137	1 HV11_MOUSE	P01755 mus musculu
10	463	30.1	138	1 HV48_MOUSE	P03380 mus musculu
11	462.5	30.1	120	1 HV50_MOUSE	P06329 mus musculu
12	462	30.1	117	1 HV12_MOUSE	P01757 mus musculu
13	457	29.8	117	1 HV13_MOUSE	P01756 mus musculu
14	446	29.0	107	1 KV6E_MOUSE	P01676 mus musculu
15	446	29.0	121	1 HV01_MOUSE	P01745 mus musculu
16	443	28.8	107	1 KV6A_MOUSE	P01675 mus musculu
17	443	28.8	117	1 KV6D_MOUSE	P01748 mus musculu
18	442	28.8	107	1 KV6D_MOUSE	P01678 mus musculu
19	441	28.7	107	1 KV6C_MOUSE	P01677 mus musculu
20	440	28.6	116	1 HV15_MOUSE	P01759 mus musculu
21	436.5	28.4	118	1 HV51_MOUSE	P06330 mus musculu
22	436	28.4	117	1 HV05_MOUSE	P01749 mus musculu
23	434	28.3	117	1 HV06_MOUSE	P01750 mus musculu
24	427	27.8	108	1 KV6K_MOUSE	P04945 mus musculu
25	426	27.7	117	1 HV09_MOUSE	P01753 mus musculu
26	424	27.6	107	1 KV6E_MOUSE	P01679 mus musculu
27	422	27.5	117	1 HV49_MOUSE	P06328 mus musculu
28	420	27.3	117	1 HV10_MOUSE	P01754 mus musculu
29	412.5	26.9	147	1 HV1C_HUMAN	P01744 homo sapien
30	411.5	26.8	117	1 HV52_MOUSE	P06327 mus musculu
31	410.5	26.7	117	1 HV14_MOUSE	P01758 mus musculu
32	407	26.5	129	1 KV4A_MOUSE	P01680 mus musculu
33	389	25.3	117	1 HV1B_HUMAN	P01743 homo sapien

34	380	24.7	117	1 HV1G_HUMAN	P23083 homo sapien
35	375.5	24.4	114	1 HV00_MOUSE	P01741 mus musculu
36	349.5	22.8	111	1 KV3M_MOUSE	P01655 mus musculu
37	346.5	22.6	108	1 KV1V_HUMAN	P04430 homo sapien
38	345.5	22.5	111	1 KV3O_MOUSE	P01667 mus musculu
39	343.5	22.4	108	1 KV1O_HUMAN	P01607 homo sapien
40	342.5	22.3	111	1 KV3L_MOUSE	P01664 mus musculu
41	339.5	22.1	111	1 KV3Q_MOUSE	P01669 mus musculu
42	338.5	22.0	108	1 KV1B_HUMAN	P01594 homo sapien
43	338.5	22.0	111	1 KV3N_MOUSE	P01666 mus musculu
44	337.5	22.0	108	1 KV1P_HUMAN	P01608 homo sapien
45	335.5	21.8	119	1 HV37_MOUSE	P01807 mus musculu

ALIGNMENTS

RESULT 1	ID	HV02_MOUSE	STANDARD;	PRT;	140 AA.
AC	P01746;	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	1g heavy chain V region 9367 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A/J;				
RX	MEDLINE=82152818; PubMed=6801765;				
RA	Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,				
RT	Capra J.D.;				
RT	"Somatic mutation in genes for the variable portion of the				
RL	immunoglobulin heavy chain.";				
CC	Science 216:309-311(1982).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	EMBL; J00493; AAA8128.1; -				
DR	PIR; A02028; HVMSG7.				
DR	HSSP; P01810; 2FBJ.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IGV; 1.				
FT	IMMUNOGLOBULIN V region; Antiarsonate antibody; Hybridoma; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.				
FT	NON TER 140 140				
SQ	SEQUENCE 140 AA; 15514 MW; 2544CBEE31DA5C8 CR664;				
Query Match	33.1%; Score 508.5; DB 1; Length 140;				
Best Local Similarity	74.4%; Pred. No. 6,9e-33;				
Matches	99; Conservative 9; Mismatches 22; Indels 3; Gaps 2;				
QY	12 LLLLAOPAM-ROVOLOOGSAGELAPGASVYKSCASGTYFTRYTMHWKORRGGLEWT 70				
DB	8 LFLSLSTAGHSEVOLOOGSAGELVPRAGSSVYKSCASGYFTFSYGINWKORRGGLEWT 67				
QY	71 GYNPGRGTYNNQKFKDKATLTFTDKSSSTAYVQWLSLTSDESAVYYCAR--YYDDHYSL 128				
DB	68 GYNPGRGTYNNQKFKDKATLTFTDKSSSTAYVQWLSLTSDESAVYYCARSHYGGSYDP 127				
QY	129 DWGCGTTLTVSS 141				

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Db 128 DYWGQGTPLTVSS 140
|||||
RESULT 2
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVM5G7.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 33.1%; Score 508; DB 1; Length 120;
Best Local Similarity 80.8%; Pred. No. 6.3e-33;
Matches 97; Conservative 5; Mismatches 16; Indels 2; Gaps 1;

Qy 24 VOLQSGAELAPGASVKMSCKASGYTFRTYTHMHWKQPGGLEWIGYINPSRGYTNVN 83
Db 1 VOLQSGAELVAGSSVKMSCKASGYTFRTSYGINVHWKQPGGLEWIGYINPENGTKYN 60
Qy 84 QKFKDKATLTDDKSSSTAYMQLSLTSDSAVYVCAR--YYDDHYSLDYWGQGTPLTVSS 141
Db 61 EKFKGKTLTVDKSSSTAYMQLSLTSDSAVYFCARSVYGGSYFYDYWGQGTPLTVSS 120

RESULT 3
HV07 MOUSE
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Inanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA

MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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CC or send an email to license@isb-sib.ch).
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DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSP; P01810; 2FBJ
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 32.8%; Score 503.5; DB 1; Length 139;
Best Local Similarity 74.8%; Pred. No. 1.7e-32;
Matches 101; Conservative 9; Mismatches 18; Indels 7; Gaps 3;

Qy 12 LLLAAQP--AMAOVLQSGAELAPGASVKMSCKASGYTFRTYTHMHWKQPGGLEW 69
Db 7 MLFLAATATGVHSQVQLQPGAEIVKPGASVLSCKASGYTFRTYTHMHWKQPGGLEW 66
Qy 70 IGYINPSRGYTNQKPKDKATLTDDKSSSTAYMQLSLTSDSAVYVCARYDDHYS-- 127
Db 67 IGRIDPNSGGTKYNEKPKSKATLTVDKPSSTAYMQLSLTSDSAVYVCARY--DYGGSS 124
Qy 128 -LDYWGQGTPLTVSS 141
Db 125 YFDYWGQGTPLTVSS 139

RESULT 4
KV6F MOUSE
ID KV6F MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGH response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 33 Seconds
(without alignments)
1816.961 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MXYLLPTAAAGLLLAQPA.....GSBQKLISEDLNHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

T number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630.5	44.9	298	11	Q9QYF0 mus musculus
2	602.5	39.2	241	11	Q921A6 mus musculus
3	551	35.9	218	11	Q925S1 mus musculus
4	531	34.6	119	5	Q9GYZ2 schistosoma
5	523	34.0	278	11	Q921K1 mus musculus
6	510	33.2	473	11	Q991K25 mus musculus
7	508	33.1	134	11	Q8VDD0 mus musculus
8	505	32.9	235	11	Q91W12 mus musculus
9	503	32.7	473	11	Q9B1A mus musculus
10	501.5	32.5	143	11	Q924R0 mus musculus
11	499.5	32.5	145	11	Q924R4 mus musculus
12	499.5	32.5	145	11	Q924O7 mus musculus
13	499	32.5	140	11	Q924P8 mus musculus
14	498	32.4	142	11	Q924Q1 mus musculus
15	498	32.4	463	11	Q991C4 mus musculus
16	497.5	32.4	143	11	Q924P9 mus musculus

17	496.5	32.3	143	11	Q91V67 mus musculus
18	496	32.3	146	11	Q924R8 mus musculus
19	495.5	32.3	145	11	Q924R1 mus musculus
20	494	32.2	146	11	Q924Q3 mus musculus
21	492.5	32.1	143	11	Q924O5 mus musculus
22	492.5	32.1	145	11	Q924O6 mus musculus
23	490.5	31.9	145	11	Q924Q9 mus musculus
24	488.5	31.8	137	11	Q924R6 mus musculus
25	487.5	31.7	141	11	Q924Q4 mus musculus
26	486.5	31.7	145	11	Q924P7 mus musculus
27	484.5	31.5	145	11	Q924R3 mus musculus
28	484	31.5	140	11	Q924R2 mus musculus
29	483	31.4	144	11	Q924P5 mus musculus
30	480.5	31.3	143	11	Q924Q0 mus musculus
31	480.5	31.3	146	11	Q991L3 mus musculus
32	477	31.1	117	11	Q9QXF0 mus musculus
33	477	31.1	117	11	Q9QXE9 mus musculus
34	474.5	30.9	146	11	Q924O8 mus musculus
35	474.5	30.9	481	11	Q91WT1 mus musculus
36	473	30.8	142	11	Q924Q2 mus musculus
37	471	30.7	168	11	Q8VDC9 mus musculus
38	468.5	30.5	143	11	Q924R7 mus musculus
39	467.5	30.4	109	11	Q91L75 mus musculus
40	463.5	30.2	143	11	Q91VA2 mus musculus
41	462.5	30.1	118	11	Q921C4 mus musculus
42	460.5	30.0	143	11	Q924P6 mus musculus
43	460	29.9	489	11	Q8VXC4 mus musculus
44	458	29.8	613	11	Q8VXC7 mus musculus
45	456.5	29.7	139	11	Q924R5 mus musculus

ALIGNMENTS

RESULT 1					
Q9QYF0	PRELIMINARY;	PRT;	298 AA.		
AC Q9QYF0;					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE CN 8 scfv.					
GN CN 8.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=BALB/C; TISSUE=SPLEEN;					
RX MEDLINE=20183931; PubMed=10706631;					
RA Shiohara N., Demura T., Fukuda H.;					
RT "Isolation of a vascular cell wall-specific monoclonal antibody					
RT recognizing a cell polarity by using a phage display subtraction					
RT method."					
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).					
DR EMBL; AB016341; BAA8633.1; -					
DR HSSP; P01607; IRET.					
DR InterPro; IPR003006; Ig_MHC.					
DR InterPro; IPR003596; Ig_V.					
DR Pfam; PF00447; Ig_2.					
DR SMART; SM00406; IGV; 2.					
SO SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;					
Query Match	44.9%;	Score 630;	DB 11;	Length 298;	
Best Local Similarity	54.7%;	Pred. No. 4,8e-46;			
Matches 139;	Conservative 35;	Mismatches 72;	Indels 8;	Gaps 5;	
QY 16 AAQPAAYVLOOQSGAEIARPGASVMSCKASGYTFRTYTMHWVKRPPQGGIEWGYNP 75					
DB 33 AAQPAAYVLOOQSGAEIARPGASVMSCKASGYTFRTYTMHWVKRPPQGGIEWGYNP 92					
QY 76 SRGYTNVQKFKDKATLTITDKSSSTAYMQLSSITSEDSAVVYCAR--VYDDHYSIDYMQQ 133					

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 39 Seconds
(without alignments)
994.255 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MKYLLPTAAAGLLLAQPA.....GSEQKISEEDINSHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

T number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1354	88.2	539	21	AA550823
2	1346.5	87.7	554	21	AA550822
3	1300.5	84.7	288	19	AAW82482
4	1208.5	78.7	288	19	AAW82316
5	1208.5	78.7	288	19	AAW82317
6	1132	73.7	409	23	AB807680
7	1132	73.7	531	21	AA43749
8	1124	73.2	495	23	AAE22193
9	1010.5	65.8	281	20	AAW82744
10	999.5	65.1	330	22	AAW70842

11	974	63.4	246	15	AAW60522	Anti-TNF diadomy D
12	964.5	62.8	309	22	AAW70841	SNV-env leader/hum
13	963.5	62.7	239	21	AAW12563	Anti-TAC sfv prote
14	963.5	62.7	239	22	AAW36826	Anti-TAC sfv prote
15	957.5	62.3	599	19	AAW37132	Anti-Tac(fv) -PE40
16	957.5	62.3	599	21	AAW87477	Anti-Tac(fv) -PE40
17	952.5	62.0	599	20	AAW95462	Anti-Tac(fv) -PE40
18	947	61.7	288	20	AAW82743	Fusion protein pMG
19	942.5	61.4	258	22	AAW82898	Anti-P53 common mu
20	940	61.2	291	22	AAW20443	Antibody 8860-amyC-
21	933.5	60.8	256	22	AAW82897	Anti-P53 common mu
22	928.5	60.4	270	16	AAW75119	MEP-23 antibody.
23	919	59.8	244	16	AAW79687	Anti-EGFR single c
24	918	59.8	305	21	AAW59265	Anti-EGFR single c
25	918	59.8	305	21	AAW51142	Murine derived pro
26	916	59.6	242	16	AAW79872	Anti-EGFR single c
27	914.5	59.5	423	22	AAW30695	A fusion of anti-C
28	912	59.4	267	20	AAW85688	Humanised Dp10 sc
29	911	59.3	244	16	AAW79873	Anti-EGFR single c
30	908	59.1	246	16	AAW79869	Anti-EGFR single c
31	905	58.9	244	16	AAW79868	Anti-EGFR single c
32	904	58.9	241	20	AAW76197	Anti-mesothelin sc
33	904	58.9	241	22	AAW50019	Antimesothelin ant
34	901.5	58.7	483	19	AAW82315	Chimeric CD19/CTCR
35	901	58.7	242	16	AAW79870	Anti-EGFR single c
36	898	58.5	553	18	AAW11508	Single chain anti-
37	898	58.5	553	20	AAW73223	H22-anti-CEA antib
38	898	58.5	553	22	AAW85455	Bi-specific single
39	898	58.5	553	22	AAW61960	Bi-specific single
40	896.5	58.4	322	22	AAW20440	Antibody 8860 biva
41	895.5	58.3	281	19	AAW82314	Human ScFvCD19 pro
42	894	58.2	276	20	AAW90227	Anti-B7.1/anti-B7.
43	889.5	57.9	271	17	AAW02293	FvKc-II-KEX2. Chi
44	888.5	57.8	242	19	AAW53881	Firefly Luciferase
45	886	57.7	242	16	AAW79871	Anti-EGFR single c

ALIGNMENTS

RESULT 1	AA550823	
ID	AA550823	standard; Protein; 539 AA.
XX		
AC	AA550823;	
XX		
DT	18-FEB-2000	(first entry)
XX		
DE	Fv-antibody construct containing antibody 9E10 epitope protein.	
XX		
KW	Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;	
KW	diagnosis; therapy; disease.	
XX		
OS	Synthetic.	
XX		
PN	DE19819846-A1.	
XX		
PD	11-NOV-1999.	
XX		
PF	05-MAY-1998;	98DE-1019846.
XX		
PR	05-MAY-1998;	98DE-1019846.
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX		
PI	Little M, Kipriyanov S;	
XX		
DR	WPI; 2000-024472/03.	
XX		
DR	N-PSDB; AA43432.	
XX		
PT	Multivalent Fv-antibody constructs with at least four variable domains	
XX	connected by 1, 2 and 3 peptide linkers	

Example 1; Fig 6; 14pp; German.

PS This invention describes a novel multivalent Fv-antibody construct with
 XX at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence represents a trivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-SL
 XX
 XX Sequence 539 AA;

Query Match 88.2%; Score 1354; DB 21; Length 539;
 Best Local Similarity 52.9%; Pred. No. 6.2e-80;
 Matches 285; Conservative 2; Mismatches 4; Indels 248; Gaps 3;
 QY 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWK 60
 DB 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWK 60
 QY 61 QPQGGLEWIGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 DB 61 QPQGGLEWIGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 QY 121 YYDDHSLDYWGQGTTLTVSSAKTPKL----- 148
 DB 121 YYDDHSLDYWGQGTTLTVSSAKTPKLGGDILLTQTPASLAVSLGORATISCKASQSV 180
 QY 149 ----- 148
 DB 181 YDGD SYLNWYQIQPGPPKLLIYDASNLVSGIPPRFSGSGSGTDFTLNHPVEKVDAA 240
 QY 149 ----- 148
 DB 241 HCQSTEDPWTGGGKLEIKRADAAGGPGSQVLOQSGAELVRPGSSVKISCKASGY 300
 QY 149 -----EGEF----- 153
 DB 301 APSSYMNWVKORPGGLEWIGIWPFGDGTNYNGKFKGKATLTADSSSTAYMQLSSLA 360
 QY 154 -----SEARV----- 172
 DB 361 SEDSAVFCARRETTTGVRYVYAMDYWGQGTSTVTSVSSAKTPKLGGDIVLTQSPALMS 420
 QY 173 PQEKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVPAPHFRGSGSGTSSYSLTI 232
 DB 421 PQEKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVPAPHFRGSGSGTSSYSLTI 480
 QY 233 SCWEAEDAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLISEEDLNHHHHH 291
 DB 481 SCWEAEDAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLISEEDLNHHHHH 539

RESULT 2

AAV50822
 ID AAV50822 standard; Protein; 554 AA.

XX AC AAV50822;
 XX DT 18-FEB-2000 (first entry)
 XX DE Fv-antibody construct containing antibody 9E10 epitope protein.
 XX KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
 XX diagnosis; therapy; disease.
 XX OS Synthetic.
 XX PN DE19819846-A1.
 XX PD 11-NOV-1999.

XX 05-MAY-1998; 98DE-1019846.
 PF 05-MAY-1998; 98DE-1019846.
 PR (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX Little M, Kipriyanov S;
 XX WPI; 2000-024472/03.
 DR N-PSDB; AAZ43431.
 XX Multivalent Fv-antibody constructs with at least four variable domains
 PT connected by 1, 2 and 3 peptide linkers
 XX Example 1; Fig 5; 14pp; German.
 XX This invention describes a novel multivalent Fv-antibody construct with
 CC at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence represents a bivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-LL
 XX
 XX Sequence 554 AA;

Query Match 87.7%; Score 1346.5; DB 21; Length 554;
 Best Local Similarity 51.4%; Pred. No. 1.9e-79;
 Matches 285; Conservative 2; Mismatches 4; Indels 263; Gaps 3;
 QY 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWK 60
 DB 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWK 60
 QY 61 QPQGGLEWIGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 DB 61 QPQGGLEWIGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 QY 121 YYDDHSLDYWGQGTTLTVSSAKTPKL----- 148
 DB 121 YYDDHSLDYWGQGTTLTVSSAKTPKLGGDILLTQTPASLAVSLGORATISCKASQSV 180
 QY 149 ----- 148
 DB 181 YDGD SYLNWYQIQPGPPKLLIYDASNLVSGIPPRFSGSGSGTDFTLNHPVEKVDAA 240
 QY 149 ----- 148
 DB 241 HCQSTEDPWTGGGKLEIKRADAAGGPGSQVLOQSGAELVRPGSSVKISCKASGY 300
 QY 149 -----EGEF----- 153
 DB 301 APSSYMNWVKORPGGLEWIGIWPFGDGTNYNGKFKGKATLTADSSSTAYMQLSSLA 360
 QY 154 -----SEARV----- 172
 DB 361 SEDSAVFCARRETTTGVRYVYAMDYWGQGTSTVTSVSSAKTPKLGGDIVLTQSPALMS 420
 QY 159 DIVLTQSPALMSAPGKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVP 217
 DB 421 DIVLTQSPALMSAPGKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVP 480
 QY 218 HFRGSGSGTSSYSLTISGMEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLI 277
 DB 481 HFRGSGSGTSSYSLTISGMEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLI 540
 QY 278 ISEEDLNHHHHH 291
 DB 541 ISEEDLNHHHHH 554

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:21:03 ; Search time 12 Seconds

(without alignments)
470.476 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MYLLPTAAGLLLAQPA.....GSEQLISEEDLNHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

T number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	872.5	56.8	239	10	US-09-808-037-6 Sequence 6, Appl1
2	858	55.9	240	10	US-09-976-787-28 Sequence 28, Appl1
3	858	55.9	240	10	US-09-865-198-27 Sequence 29, Appl1
4	850	55.3	238	10	US-09-976-787-29 Sequence 29, Appl1
5	850	55.3	238	10	US-09-865-198-28 Sequence 28, Appl1
6	817.5	53.2	268	10	US-09-818-247-22 Sequence 22, Appl1
7	813.5	53.0	260	10	US-09-811-737-16 Sequence 16, Appl1
8	809.5	52.7	260	10	US-09-811-737-17 Sequence 17, Appl1
9	763.5	49.7	669	9	US-09-807-721-2 Sequence 2, Appl1
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11	724	47.1	249	10	US-09-984-186-18 Sequence 18, Appl1
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13	710	46.2	243	10	US-09-924-099-10 Sequence 10, Appl1
14	707	46.0	255	10	US-09-811-737-15 Sequence 15, Appl1
15	706.5	46.0	267	10	US-09-766-543-10 Sequence 10, Appl1
16	696.5	45.3	245	9	US-09-991-470-27 Sequence 27, Appl1
17	690.5	45.0	535	9	US-09-968-851-38 Sequence 38, Appl1
18	689	44.9	252	9	US-09-887-853-4 Sequence 4, Appl1
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21	667.5	43.5	270	10	US-09-976-118-2 Sequence 2, Appl1
22	662.5	43.1	276	10	US-09-766-543-12 Sequence 12, Appl1
23	656.5	42.7	240	9	US-09-968-561A-2 Sequence 2, Appl1
24	656.5	42.7	240	10	US-09-192-854-2 Sequence 2, Appl1
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28	640.5	41.7	269	12	US-10-027-770-5 Sequence 5, Appl1
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39	606.5	39.5	296	10	US-09-888-721-42 Sequence 42, Appl1
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41	599	39.0	249	10	US-09-730-374-3 Sequence 3, Appl1
42	598	38.9	245	12	US-10-039-785-46 Sequence 46, Appl1
43	587	38.9	381	10	US-09-822-698A-5 Sequence 5, Appl1
44	582	37.9	245	12	US-10-039-785-42 Sequence 42, Appl1
45	582	37.9	245	12	US-10-039-785-43 Sequence 43, Appl1

ALIGNMENTS

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US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: HANAN, Bilal
; APPLICANT: SOLOMON, Beke
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON:2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6
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Query Match 56.8%; Score 872.5; DB 10; Length 239;

Best Local Similarity 71.4%; Pred. No. 7.8e-42;
Matches 177; Conservative 13; Mismatches 41; Indels 17; Gaps 3;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: January 12, 2003, 10:19:49 ; Search time 15 Seconds

(without alignments)
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Title: US-09-424-705B-2

Perfect score: 1536

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Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	963.5	62.7	239	4	US-08-902-486-11
6	957.5	62.3	599	1	US-08-463-163-3
7	947	61.7	288	4	US-09-423-439-38
8	928.5	60.4	270	2	US-08-652-507-2
9	919	59.8	244	4	US-08-553-497A-20
10	912	59.4	267	2	US-09-485-737B-2
11	908	59.1	246	2	US-08-553-497A-24
12	905	58.9	244	2	US-08-553-497A-22
13	901	58.7	242	2	US-08-553-497A-26
14	898	58.5	553	4	US-08-661-052-16
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19	886	57.7	242	2	US-08-553-497A-28
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27	813	52.9	235	4	US-09-485-737B-93

28	808	52.6	541	4	US-09-485-737B-85	Sequence 85, Appl
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30	788.5	51.3	252	2	US-08-894-922A-14	Sequence 14, Appl
31	788	51.3	269	2	US-08-428-257A-72	Sequence 72, Appl
32	788	51.3	269	2	US-08-491-988-3	Sequence 3, Appl
33	788	51.3	402	2	US-08-491-988-9	Sequence 9, Appl
34	788	51.3	415	2	US-08-491-988-7	Sequence 7, Appl
35	788	51.3	435	2	US-08-491-988-5	Sequence 5, Appl
36	783.5	51.0	236	2	US-08-190-199A-65	Sequence 65, Appl
37	781	50.8	711	4	US-09-485-737B-90	Sequence 90, Appl
38	776.5	50.6	240	2	US-08-800-198-8	Sequence 8, Appl
39	776.5	50.6	240	3	US-09-296-595-8	Sequence 8, Appl
40	773.5	50.4	222	2	US-08-190-199A-67	Sequence 67, Appl
41	771.5	50.2	240	2	US-08-956-047-25	Sequence 25, Appl
42	770.5	50.2	269	4	US-08-646-265A-109	Sequence 109, Appl
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44	761	49.5	235	2	US-08-190-199A-61	Sequence 61, Appl
45	752	49.0	553	2	US-08-263-911-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-423-439-44
; Sequence 44, Application US/09423439
; Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKELY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423 439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44
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Best Local Similarity 70.4%; Pred. No. 3.3e-70;
Matches 205; Conservative 20; Mismatches 55; Indels 11; Gaps 3;
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; Sequence 57, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holteet, Ihor Las
; APPLICANT: Eterodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-658-57

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Best Local Similarity 74.5%; Pred. No. 1.8e-67;
Matches 196; Conservative 17; Mismatches 32; Indels 18; Gaps 4

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GenCore version 5.1.3
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and is derived by analysis of the total score distribution.

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ACCESSION AX011208
VERSION AX011208.1 GI:9997788
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1653)
AUTHORS Kipriyanov,S. and Little,M.
TITLE Multivalent antibody constructs
JOURNAL Patent: WO 9957150-A 3 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
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LAVSLGORATISCKASQSDYDGSYLNWYQOIPGQPKLLIYDASNLVSGIPRFFSG
SGSGTDFTLNIHPVEKYDAATYHCQQTEDPWFQGGTKEIKRADAAAGGSGSQVQ
LQSGAELVRPGSSVKIICKASGYAFSSYMMWVKORPGGLEWIGQIPWGDGTNYN
GKFGKATLTADESSSTAYMQLSLASDSAVYFCARRETTTVGRYYVAMDYWGQGTG
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BASE COUNT 432 a 429 c 424 g 368 t
ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 1653;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGTCAAGGCTGTAATGATCATC 24
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Db 417 GTAGTCAAGGCTGTAATGATCATC 394
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RESULT 2
AX011206/c
LOCUS AX011206 1698 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9957150.
ACCESSION AX011206
VERSION AX011206.1 GI:9997786
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1698)
AUTHORS Kipriyanov,S. and Little,M.
TITLE Multivalent antibody constructs
JOURNAL Patent: WO 9957150-A 1 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
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FEATURES
source Location/Qualifiers
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/db_xref="GI:9997787"
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SGSGTDFTLNIHPVEKYDAATYHCQQTEDPWFQGGTKEIKRADAAAGGSGSGG
GSGGSGGSGSQVLOQSGAELVRPGSSVKIICKASGYAFSSYMMWVKORPGQGLE
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGTCAAGGCTGTAATGATCATC 24
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Db 417 GTAGTCAAGGCTGTAATGATCATC 394
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RESULT 3
AL133510/c
LOCUS AL133510 122680 bp DNA linear PRI 01-MAR-2001
DEFINITION Human DNA sequence from clone RP3-481C9 on chromosome 6q25.1-26,
complete sequence.
ACCESSION AL133510
VERSION AL133510.13 GI:13160149
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 768 Seconds
(without alignments)
506.109 Million cell updates/sec

Title: US-09-424-705B-7

Perfect score: 24

Sequence: 1 gtagtcaagctgtaatgcatc 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

W size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

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 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
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 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estrom:*
 - 17: gb_gse:*
 - 18: em_gse_hum:*
 - 19: em_gse_inv:*
 - 20: em_gse_pin:*
 - 21: em_gse_vit:*
 - 22: em_gse_fun:*
 - 23: em_gse_mam:*
 - 24: em_gse_mus:*
 - 25: em_gse_other:*
 - 26: em_gse_pro:*
 - 27: em_gse_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	70.8	278	9	A1632464
C 2	17	70.8	278	10	AM594601
C 3	17	70.8	657	10	BB634155
C 4	17	70.8	661	10	BB207696
C 5	17	70.8	702	10	AW442262
C 6	16	66.7	183	12	BF925395

C 7	16	66.7	264	12	BF746269	BF746269 RCL-BT025
C 8	16	66.7	264	12	BF746339	BF746339 RCL-BT025
C 9	16	66.7	304	9	AA658135	AA658135 nml16g12.s
C 10	16	66.7	316	14	F12222	F12222 HSC37C031 n
C 11	16	66.7	325	12	BF926184	BF926184 CM2-NT019
C 12	16	66.7	337	17	AQ213370	AQ213370 HS-3048-B
C 13	16	66.7	443	9	A1184601	A1184601 qf46a10.x
C 14	16	66.7	503	17	A2517652	A2517652 RPL1-11-2
C 15	16	66.7	505	14	BQ248981	BQ248981 TAE25001F
C 16	16	66.7	515	14	T66349	T66349 yc78c03.r1
C 17	16	66.7	540	12	BF615532	BF615532 de08d09.y
C 18	16	66.7	583	17	A0584576	A0584576 RPL1-11-4
C 19	16	66.7	657	17	A2384732	A2384732 LM0142D24
C 20	16	66.7	666	14	BM998944	BM998944 UI-R-DIO-
C 21	16	66.7	676	17	A2396616	A2396616 IM0161C18
C 22	16	66.7	681	17	AG185106	AG185106 Pan trogl
C 23	16	66.7	785	12	BG616803	BG616803 602615939
C 24	16	66.7	1065	17	CNS058GH	A1325898 Tetraodon
C 25	16	66.7	1108	17	CNS060LN	AL110817 T7 end of
C 26	16	66.7	145	10	BE160172	BE160172 QV1-H7041
C 27	15	62.5	202	10	AM230182	AM230182 up28a05.y
C 28	15	62.5	345	12	BE722254	BE722254 190421.MA
C 29	15	62.5	347	14	T69741	T69741 yd14a03.81
C 30	15	62.5	351	17	A2762063	A2762063 IM0556C17
C 31	15	62.5	354	9	AA655771	AA655771 vs44c02.r
C 32	15	62.5	396	17	AQ093328	AQ093328 HS-3018.A
C 33	15	62.5	397	17	AQ124987	AQ124987 HS-2163.A
C 34	15	62.5	408	9	A1974599	A1974599 T113049e-
C 35	15	62.5	412	9	AA670664	AA670664 v107c05.r
C 36	15	62.5	420	10	AM210912	AM210912 u089c02.y
C 37	15	62.5	435	9	AA798226	AA798226 ubd0907.r
C 38	15	62.5	441	10	AM081157	AM081157 xc40a05.x
C 39	15	62.5	442	17	AQ312042	AQ312042 RPL11-93
C 40	15	62.5	474	17	A2802229	A2802229 2M0060L22
C 41	15	62.5	485	17	C11185	A1226198 Ciona inc
C 42	15	62.5	500	17	A2821134	A2821134 2M0093G14
C 43	15	62.5	504	17	AQ119899	AQ119899 HS-3018.A
C 44	15	62.5	522	12	BF075556	BF075556 224699.MA
C 45	15	62.5	549	17	AO459910	AO459910 HS-5131.B
C 46	15	62.5	551	12	BF073827	BF073827 220806.MA
C 47	15	62.5	560	12	BG370569	BG370569 ux71c12.y
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C 49	15	62.5	572	12	BF120318	BF120318 601756054
C 50	15	62.5	576	17	FR0030095	AL026464 Fugu rubr
C 51	15	62.5	587	12	BG834105	BG834105 352206.MA
C 52	15	62.5	588	17	A2251024	A2251024 RPL1-23-6
C 53	15	62.5	590	12	BG543031	BG543031 E0502 Chi
C 54	15	62.5	601	17	FR0030150	AL026519 Fugu rubr
C 55	15	62.5	604	17	A2862534	A2862534 2M0170G14
C 56	15	62.5	624	13	BM448293	BM448293 DSA024C03
C 57	15	62.5	636	12	BF647532	BF647532 NF076H02E
C 58	15	62.5	644	17	DR15M6T	AL1734832 Dario rer
C 59	15	62.5	658	17	A2839294	A2839294 2M0135D24
C 60	15	62.5	662	10	BB009428	BB009428 BB009428
C 61	15	62.5	668	17	AQ162354	AQ162354 m9xb0012B
C 62	15	62.5	668	12	BG228652	BG228652 ux71c12.x
C 63	15	62.5	670	17	AG052147	AG052147 Pan trogl
C 64	15	62.5	675	14	BQ255372	BQ255372 MTNAC45TK
C 65	15	62.5	681	13	BI251197	BI251197 602994403
C 66	15	62.5	682	12	BF645086	BF645086 NF020811E
C 67	15	62.5	682	12	BF165211	BF165211 601778018
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C 70	15	62.5	849	17	AQ740013	AQ740013 HS-5503.A
C 71	15	62.5	911	12	BF165103	BF165103 601778259
C 72	15	62.5	938	12	BF141897	BF141897 601791380
C 73	15	62.5	997	17	CNS0706F	AL140077 T3 end of
C 74	15	62.5	1044	12	BF578042	BF578042 602091888
C 75	15	62.5	1103	14	BM920389	BM920389 AGENCOURT
C 76	15	62.5	1313	17	BH860804	BH860804 ORNL269.P
C 77	15	62.5	1355	11	AK008855	AK008855 Mus muscu
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C 79	15	58.3	105	9	AA588295	AA588295 mms1a01.s

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90      14 58.3 244 17 BH667684 BOMFT07TR
91      14 58.3 250 9 AV013654 AV013654
92      14 58.3 250 17 AQ097325 HS_3039.B
93      14 58.3 256 17 AQ097325 HS_3039.B
94      14 58.3 265 9 AV222455 AV222455
95      14 58.3 269 10 AW854223 RC3-CT025
96      14 58.3 270 9 AA322799 EST25481
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98      14 58.3 282 17 BH870924 hm86906.b
99      14 58.3 284 13 B1436565 gc48d10.y
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ALIGNMENTS

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RESULT 1
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LOCUS      278 bp mRNA linear EST 17-DEC-1999
DEFINITION wh09d06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2305163 3'
             similar to contains Alu repetitive element, mRNA sequence.
ACCESSION  A1632464
VERSION    A1632464.1 GI:4683794
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 278)
REFERENCE  1
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
          R. Emmert-Buck, M.D., Ph.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
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              /lab_host="DH10B"
              /note="(vector: pTT73D-Pac (Pharmacia) with a modified
              polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
              from the normalized library NCI-CGAP GC4 was prepared, and
              ss circles were made in vitro. Following HAP purification,
              this DNA was used as tracer in a subtractive hybridization
              reaction. The driver was PCR-amplified cDNAs from a pool
              of 5,000 clones made from the same library (cloneIDs
              1257096-1258631, 1469064-1470983, and 1475592-1476743).
              Subtraction by Bento Soares and M. Fatima Bonaldo. "

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FEATURES
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1..278
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
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  /note="(vector: pTT73D-Pac (Pharmacia) with a modified
  polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
  from the normalized library NCI-CGAP GC4 was prepared, and
  ss circles were made in vitro. Following HAP purification,
  this DNA was used as tracer in a subtractive hybridization
  reaction. The driver was PCR-amplified cDNAs from a pool
  of 5,000 clones made from the same library (cloneIDs
  1257096-1258631, 1469064-1470983, and 1475592-1476743).
  Subtraction by Bento Soares and M. Fatima Bonaldo. "

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```

BASE COUNT 67 a 75 c 57 g 79 t
ORIGIN
Query Match 70.8%; Score 17; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGTCAAGGCTGTAATGA 19
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Db 72 AGTCAAGGCTGTAATGA 56
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RESULT 2
AW594601/c
LOCUS      278 bp mRNA linear EST 22-MAR-2000
DEFINITION hg67d06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2950667 3'
             similar to contains Alu repetitive element, mRNA sequence.
ACCESSION  AW594601
VERSION    AW594601.1 GI:7281951
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 278)
REFERENCE  1
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
          R. Emmert-Buck, M.D., Ph.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
          Bonaldo, Ph.D.
          CDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          image.llnl.gov/image/html/iresources.shtml
          Seq primer: -40UP from Gibco.
          Location/Qualifiers
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              /note="(vector: pTT73D-Pac (Pharmacia) with a modified
              polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
              from the normalized library NCI-CGAP GC4 was prepared, and
              ss circles were made in vitro. Following HAP purification,
              this DNA was used as tracer in a subtractive hybridization
              reaction. The driver was PCR-amplified cDNAs from a pool
              of 5,000 clones made from the same library (cloneIDs
              1257096-1258631, 1469064-1470983, and 1475592-1476743).
              Subtraction by Bento Soares and M. Fatima Bonaldo. "

```

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BASE COUNT 67 a 75 c 57 g 79 t
ORIGIN
Query Match 70.8%; Score 17; DB 10; Length 278;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 72 AGTCAAGGCTGTAATGA 56
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RESULT 3
BB634155
LOCUS      657 bp mRNA linear EST 26-OCT-2001

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 96.7317 Seconds
(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-7

Perfect score: 24
Sequence: 1 gtagcgaagcgtcaatgcatcac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wc size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

1: N_Geneseq_101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	AAV73336	Mouse OKT3 variant
2	24	100.0	898	AAV73335	Mouse OKT3 variant
3	24	100.0	1653	AAZ43432	Fv-antibody constr
4	24	100.0	1698	AAZ43431	Fv-antibody constr
5	24	100.0	1794	AAV73337	Mouse bispecific a
6	16	66.7	346	AA537402	Novel human diagn
7	16	66.7	487	AA181103	Human polynucleoti
8	16	66.7	13024	AA104739	Human reproductive
9	16	66.7	13024	ABL97644	Human testicular a

10	16	66.7	22651	AAK78202	Human immune/haema
11	16	66.7	28180	AAK68939	Human immune/haema
12	15	62.5	17	AAF57365	Murine Cdc25A intr
13	15	62.5	261	AAK27376	Human secreted pro
14	15	62.5	431	ABV16978	Human prostate exp
15	15	62.5	441	AAK75439	Human prostate exp
16	15	62.5	441	AAK75440	Human immune/haema
17	15	62.5	478	ABV46773	Human immune/haema
18	15	62.5	545	AAK30815	Human prostate exp
19	15	62.5	654	AAK98657	Streptococcus pneu
20	15	62.5	1428	AAA05441	DNA encoding a S.
21	15	62.5	2690	AAK59990	Streptococcus pneu
22	15	62.5	12665	AAV52267	Glucose repressor
23	15	62.5	21429	AAF57362	Streptococcus pneu
24	15	62.5	30175	AAD32742	Murine Cdc25A comp
25	15	62.5	59060	AAK85994	Human drug metabol
26	15	62.5	109906	ABK94411	Human immune/haema
27	14	58.3	225	ABN91407	DNA encoding endo
28	14	58.3	354	AAAF6037	Staphylococcus epi
29	14	58.3	587	AAAF08479	Pseudomonas ppqf g
30	14	58.3	608	AAD00428	Fusarium venenatum
31	14	58.3	680	AAD17148	Human MINT10 DNA c
32	14	58.3	861	ABK78815	Human ion channel-
33	14	58.3	954	ABK78815	Bacillus clausii g
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35	14	58.3	1392	AAK37583	Arabidopsis thalia
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37	14	58.3	1393	AAK50697	Propionibacterium
38	14	58.3	1443	AAH68451	Arabidopsis thalia
39	14	58.3	1446	AAH68451	C glutamicum codin
40	14	58.3	1566	AAQ52852	Theonine synthase
41	14	58.3	1708	AAAF71840	Corynebacterium gl
42	14	58.3	1760	AAAC61445	Human polynucleoti
43	14	58.3	1981	AAAC4674	Zea mays DNA fragm
44	14	58.3	2007	AAI58359	Human bromine grou
45	14	58.3	2242	AAH02744	Human polynucleoti
46	14	58.3	2247	AAH02744	Prostate tumour an
47	14	58.3	2247	AAH02744	Human P714P invent
48	14	58.3	2247	AAH02744	Human P714P CDNA s
49	14	58.3	2247	AAH02744	Streptococcus pneu
50	14	58.3	2247	AAH02744	Human prostate spe
51	14	58.3	2247	AAH02744	Human prostate spe
52	14	58.3	2247	AAH02744	Human prostate spe
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71	14	58.3	2247	AAH02744	Human prostate spe
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80	14	58.3	2247	AAH02744	Human prostate spe
81	14	58.3	2247	AAH02744	Human prostate spe
82	13	54.2	65	ABN52848	Mouse spliced tran

Human immune/haema
Human immune/haema
Murine Cdc25A intr
Human secreted pro
Human prostate exp
Human prostate exp
Human immune/haema
Human immune/haema
Human prostate exp
Streptococcus pneu
DNA encoding a S.
Streptococcus pneu
Glucose repressor
Streptococcus pneu
Murine Cdc25A comp
Human drug metabol
Human immune/haema
DNA encoding endo
Staphylococcus epi
Pseudomonas ppqf g
Fusarium venenatum
Human MINT10 DNA c
Human ion channel-
Bacillus clausii g
Staphylococcus epi
Arabidopsis thalia
Arabidopsis thalia
Propionibacterium
Arabidopsis thalia
C glutamicum codin
Theonine synthase
Corynebacterium gl
Human polynucleoti
Zea mays DNA fragm
Human bromine grou
Human polynucleoti
Human amyloid prec
Human immunogenic
Human prostate CDN
Human prostate spe
Human prostate spe
Human prostate spe
Prostate tumour an
Human P714P invent
Human P714P CDNA s
Streptococcus pneu
Human CDNA sequenc
Human polynucleoti
Human nervous syst
Clone contg. thrc
CDNA encoding nove
Human polynucleoti
Human prostate exp
Human prostate exp
Human prostate exp
Human prostate exp
S. epidermidis gen
Human RalGDS (hral
Human prostate CDN
P714P extended CDN
Human P714P CDNA s
Drosophila melanog
Carbonic anhydrase
Propionibacterium
Propionibacterium
Pgi genomic coding
Wild type Pgi codi
C glutamicum codin
Genomic sequence o
Mouse spliced tran

83 13 54.2 73 16 AAT25114 Human gene signatu
 84 13 54.2 96 21 AAC12679 Human secreted pro
 85 13 54.2 156 19 AAV33544 Clone 132750 cDNA
 86 13 54.2 183 23 AAS50445 Staphylococcus aur
 87 13 54.2 201 24 AAD33411 Human organic anio
 88 13 54.2 217 20 AAH86987 Human single nucle
 89 13 54.2 227 18 AAX83372 Breast cancer tumo
 90 13 54.2 227 19 AAV68911 DNA molecule encod
 91 13 54.2 227 21 AAC80895 Human breast tumou
 92 13 54.2 227 24 ABK46785 Human breast tumou
 93 13 54.2 227 24 AAS99741 Breast tumour-spec
 94 13 54.2 229 20 AAV86596 EST clone BG48. H
 95 13 54.2 251 19 AAX11171 Human biallelic po
 96 13 54.2 251 19 AAX11172 Human biallelic po
 97 13 54.2 279 23 ABV57833 Human prostate exp
 98 13 54.2 289 23 AAS49767 Staphylococcus aur
 99 13 54.2 289 23 AAS49786 Staphylococcus aur
 100 13 54.2 289 23 AAS49792 Staphylococcus aur

ALIGNMENTS

RESULT 1
 AAV73336
 ID AAV73336 standard; DNA; 24 BP.
 AC AAV73336;
 DT 26-FEB-1999 (first entry)
 XX Mouse OKT3 variant antibody primer SK1 DNA.
 DE OKT3; monoclonal antibody; MAB; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; primer; ss.
 XX Synthetic.
 OS Mus sp.
 PN DE19721700-Cl.
 PD 19-NOV-1998.
 XX 23-MAY-1997; 97DE-1021700.
 PF 23-MAY-1997; 97DE-1021700.
 PR 23-MAY-1997; 97DE-1021700.
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI; 1998-596150/51.
 DR Monoclonal antibody OKT3 with point-mutation - where cysteine is
 XX replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 PS Claim 7; Column 3; 8pp; German.
 CC This sequence is a primer used in the construction of a monoclonal
 CC antibody (MAB) derived from OKT3 with a point-mutation where Cys at
 CC position H100A is replaced with another polar amino acid, in this example
 CC Ser. The MAB is used in lowering or eliminating the transplant rejection
 CC in an organ recipient and for diagnostic methods for tumours and tumour
 CC therapy.
 XX Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 24; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTAGTCAAGGCTGTAATGATCATC 24

Db 1 GTAGTCAAGGCTGTAATGATCATC 24
 RESULT 2
 AAV73335/c
 ID AAV73335 standard; DNA; 898 BP.
 XX AAV73335;
 AC AAV73335;
 DT 26-FEB-1999 (first entry)
 XX Mouse OKT3 variant antibody DNA.
 DE OKT3; monoclonal antibody; MAB; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; ss.
 XX Mus sp.
 OS Synthetic.
 PN DE19721700-Cl.
 PD 19-NOV-1998.
 XX 23-MAY-1997; 97DE-1021700.
 PF 23-MAY-1997; 97DE-1021700.
 PR 23-MAY-1997; 97DE-1021700.
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI; 1998-596150/51.
 DR P-PSDB; AAW82316.
 XX Monoclonal antibody OKT3 with point-mutation - where cysteine is
 PT replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 PS Claim 3; Fig 2; 8pp; German.
 CC This sequence encodes a monoclonal antibody (MAB) derived from OKT3 with
 CC a point-mutation where Cys at position H100A is replaced with another
 CC polar amino acid, in this example Ser. The MAB is used in lowering or
 CC eliminating the transplant rejection in an organ recipient, and for
 CC diagnostic methods for tumours and tumour therapy.
 XX Sequence 898 BP; 245 A; 236 C; 217 G; 200 T; 0 other;
 SQ Query Match 100.0%; Score 24; DB 19; Length 898;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTAGTCAAGGCTGTAATGATCATC 24
 Db 417 GTAGTCAAGGCTGTAATGATCATC 394
 RESULT 3
 AAZ43432/c
 ID AAZ43432 standard; DNA; 1653 BP.
 XX AAZ43432;
 AC AAZ43432;
 DT 18-FEB-2000 (first entry)
 XX Fv-antibody construct containing antibody 9E10 epitope DNA.
 DE Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
 KW diagnosis; therapy; disease; ss.
 XX Synthetic.
 OS

PN DE19819846-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1998; 98DE-1019846.
 XX
 PR 05-MAY-1998; 98DE-1019846.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Little M, Kipriyanov S;
 XX
 DR WPI; 2000-024472/03.
 XX
 PT Multivalent Fv-antibody constructs with at least four variable domains
 PT connected by 1, 2 and 3 peptide linkers -
 XX
 PS Example 1; Fig 6; 14pp; German.
 XX
 CC This invention describes a novel multivalent Fv-antibody construct with
 CC at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence encodes a tetraivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-IL
 XX
 SQ Sequence 1653 BP; 432 A; 429 C; 424 G; 368 T; 0 other;
 XX
 QY
 1 GTAGTCAAGGCTGTAATGATCATC 24
 |||||
 417 GTAGTCAAGGCTGTAATGATCATC 394
 Db
 RESULT 4
 AA243431/c
 ID AA243431 standard; DNA; 1698 BP.
 XX
 AC AA243431;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 D Fv-antibody construct containing antibody 9E10 epitope DNA.
 XX
 KM Multivalent; Fv-antibody; antiviral, antibacterial; cytostatic;
 KM diagnosis; therapy; disease; ss.
 XX
 OS Synthetic.
 XX
 PN DE19819846-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1998; 98DE-1019846.
 XX
 PR 05-MAY-1998; 98DE-1019846.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Little M, Kipriyanov S;
 XX
 DR WPI; 2000-024472/03.
 XX
 DR P-PSDB; AAY50822.
 XX
 PT Multivalent Fv-antibody constructs with at least four variable domains
 PT connected by 1, 2 and 3 peptide linkers -
 XX

PS Example 1; Fig 5; 14pp; German.
 XX
 CC This invention describes a novel multivalent Fv-antibody construct with
 CC at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence encodes a bivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-IL
 XX
 SQ Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 other;
 XX
 QY
 1 GTAGTCAAGGCTGTAATGATCATC 24
 |||||
 417 GTAGTCAAGGCTGTAATGATCATC 394
 Db
 RESULT 5
 AA73337/c
 ID AA73337 standard; DNA; 1794 BP.
 XX
 AC AA73337;
 XX
 DT 26-FEB-1999 (first entry)
 XX
 D Mouse bispecific antibody construct variant OKT3/anti-CD19 DNA.
 XX
 DE OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19;
 KW anti-CD3; ss.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 OS Key Location/Qualifiers
 FH CDS 28..894
 FT /*tag= a
 FT /product= "mutant OKT3 with anti-CD19 insert"
 FT CDS 922..1788
 FT /*tag= b
 FT /product= "mutant OKT3 with anti-CD3 insert"
 XX
 PN DE19721700-C1.
 XX
 PD 19-NOV-1998.
 XX
 PF 23-MAY-1997; 97DE-1021700.
 XX
 PR 23-MAY-1997; 97DE-1021700.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX
 DR WPI; 1998-596150/51.
 XX
 DR P-PSDB; AAW82317, AAW82482.
 XX
 PT Monoclonal antibody OKT3 with point-mutation - where cysteine is
 PT replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 XX
 PS Disclosure; Fig 3; 8pp; German.
 XX
 CC This sequence encodes a monoclonal antibody (MAb) diabody derived from
 CC OKT3 with a point-mutation where Cys at position H100A is replaced with
 CC another polar amino acid, in this example Ser. The diabody encodes two
 CC OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3

CC activity. The MAb is used in lowering or eliminating the transplant
CC rejection in an organ recipient and for diagnostic methods for tumours
CC and tumour therapy.
XX
SQ Sequence 1794 BP; 480 A; 468 C; 450 G; 396 T; 0 other;
Query Match 100.0%; Score 24; DB 19; Length 1794;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGTCAAGGCTGTAATGATC 24
|||||
Db 417 GTAGTCAAGGCTGTAATGATC 394
|||||

RESULT 6
AAS37402
ID AAS37402 standard; cDNA; 346 BP.
XX
AC AAS37402;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #460.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US07787.
XX
PR 09-MAR-2000; 2000US-0188609.
XX
PA (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX WPI; 2001-530177/58.
DR
XX New polynucleotides and polypeptides, useful for diagnosis and
PT treatment of breast, lung and colon cancer -
PT
XX Claim 1; Page 712; 1193pp; English.
XX
XX The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention.
XX
SQ Sequence 346 BP; 112 A; 67 C; 87 G; 79 T; 1 other;
Query Match 66.7%; Score 16; DB 22; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATGA 19
|||||
Db 320 GTCAAGGCTGTAATGA 335
|||||

RESULT 7
AAI81103/c
ID AAI81103 standard; cDNA; 487 BP.
XX
AC AAI81103;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1163.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX
DR P-PSDB; AAO01172.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 1163; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 487 BP; 125 A; 128 C; 102 G; 130 T; 2 other;
Query Match 66.7%; Score 16; DB 22; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATGA 19
|||||
Db 412 GTCAAGGCTGTAATGA 397
|||||

RESULT 8
AAL04739
ID AAL04739 standard; DNA; 13024 BP.
XX
AC AAL04739;
XX
DT 21-NOV-2001 (first entry)
XX

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OM nucleic - nucleic search, using sw model

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Title: US-09-424-705b-7

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	62.5	30175	10	US-09-738-878-3	Sequence 3, Appl1
2	15	62.5	12	US-10-163-381-3	Sequence 3, Appl1
3	14	58.3	341	US-09-783-590-10253	Sequence 10253, A
4	14	58.3	517	US-09-783-590-358	Sequence 358, App
5	14	58.3	861	US-09-974-300-6106	Sequence 6106, Ap
6	14	58.3	1167	US-09-938-842A-1133	Sequence 1133, Ap
7	14	58.3	1443	US-09-738-826-3486	Sequence 3486, Ap
8	14	58.3	2417	US-09-232-880-334	Sequence 334, App
9	14	58.3	2417	US-10-012-896-334	Sequence 334, App
10	14	58.3	2417	US-09-895-793-334	Sequence 334, App
11	14	58.3	2417	US-09-895-814-334	Sequence 334, App
12	14	58.3	2417	US-09-759-143-334	Sequence 334, App
13	14	58.3	2417	US-09-780-669-334	Sequence 334, App
14	14	58.3	2417	US-09-822-827-334	Sequence 334, App
15	14	58.3	2709	US-09-922-199A-3	Sequence 3, Appl1
16	14	58.3	3674	US-10-012-896-698	Sequence 698, App
17	14	58.3	3674	US-09-895-793-698	Sequence 698, App
18	14	58.3	3674	US-09-895-814-698	Sequence 698, App
19	14	58.3	3674	US-09-759-143-698	Sequence 698, App

20	14	58.3	3674	10	US-09-780-669-698	Sequence 698, App
21	14	58.3	3674	10	US-09-822-827-698	Sequence 698, App
22	14	58.3	3691	9	US-09-922-199A-1	Sequence 1, Appl1
23	14	58.3	56516	9	US-09-853-526-1	Sequence 1, Appl1
24	14	58.3	56516	10	US-09-901-484A-1	Sequence 1, Appl1
25	14	58.3	56520	9	US-09-853-526-179	Sequence 179, App
26	14	58.3	56520	10	US-09-901-484A-179	Sequence 179, App
27	13	54.2	183	10	US-09-815-242-3022	Sequence 3022, Ap
28	13	54.2	201	10	US-09-925-731-11	Sequence 11, Appl1
29	13	54.2	227	9	US-09-924-400-183	Sequence 183, App
30	13	54.2	227	10	US-09-810-936-183	Sequence 183, App
31	13	54.2	227	10	US-09-429-755-183	Sequence 183, App
32	13	54.2	267	10	US-09-878-574-11257	Sequence 11257, A
33	13	54.2	271	10	US-09-878-574-11153	Sequence 11153, A
34	13	54.2	271	10	US-09-878-574-14243	Sequence 14243, A
35	13	54.2	282	10	US-09-983-965-346	Sequence 346, Ap
36	13	54.2	289	10	US-09-815-242-2344	Sequence 2344, Ap
37	13	54.2	289	10	US-09-815-242-2363	Sequence 2363, Ap
38	13	54.2	289	10	US-09-815-242-2369	Sequence 2369, Ap
39	13	54.2	289	10	US-09-815-242-2327	Sequence 3227, Ap
40	13	54.2	324	10	US-09-764-877-3392	Sequence 3392, Ap
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42	13	54.2	371	10	US-09-867-701-10550	Sequence 10550, A
43	13	54.2	398	10	US-09-983-965-184	Sequence 184, App
44	13	54.2	401	9	US-09-946-807-478	Sequence 478, App
45	13	54.2	401	10	US-09-795-668-478	Sequence 478, App
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47	13	54.2	405	9	US-09-796-692-2980	Sequence 2980, Ap
48	13	54.2	424	10	US-09-867-701-8230	Sequence 8230, Ap
49	13	54.2	432	10	US-09-960-332-2913	Sequence 2913, Ap
50	13	54.2	436	10	US-09-983-965-458	Sequence 458, App
51	13	54.2	446	10	US-09-864-761-1959	Sequence 1959, Ap
52	13	54.2	491	10	US-09-783-590-6297	Sequence 6297, Ap
53	13	54.2	521	10	US-09-864-761-8459	Sequence 8459, Ap
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55	13	54.2	572	10	US-09-864-761-16498	Sequence 16498, A
56	13	54.2	602	9	US-09-796-692-8538	Sequence 8538, Ap
57	13	54.2	699	9	US-09-738-626-921	Sequence 921, Appl
58	13	54.2	908	9	US-09-866-570A-23	Sequence 23, Appl
59	13	54.2	908	10	US-09-866-570A-23	Sequence 23, Appl
60	13	54.2	927	10	US-09-729-674-75	Sequence 75, Appl
61	13	54.2	948	10	US-09-886-055-126	Sequence 126, App
62	13	54.2	1269	10	US-09-771-161A-21	Sequence 21, Appl
63	13	54.2	1275	9	US-09-938-842A-1977	Sequence 1977, Ap
64	13	54.2	1586	10	US-09-870-962-11	Sequence 11, Appl
65	13	54.2	1827	10	US-09-925-302-270	Sequence 270, App
66	13	54.2	1885	10	US-09-764-869-2417	Sequence 2417, App
67	13	54.2	1885	10	US-09-764-869-2417	Sequence 2417, App
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70	13	54.2	2257	10	US-09-972-912-42	Sequence 42, Appl
71	13	54.2	2448	10	US-09-967-768A-187	Sequence 187, App
72	13	54.2	2632	9	US-10-108-605-36	Sequence 36, Appl
73	13	54.2	2920	10	US-09-956-004-10	Sequence 10, Appl
74	13	54.2	6331	10	US-09-925-301-536	Sequence 536, App
75	13	54.2	6331	10	US-09-764-865-183	Sequence 183, App
76	13	54.2	6331	10	US-09-764-865-183	Sequence 183, App
77	13	54.2	8472	9	US-09-764-868-1306	Sequence 1306, Ap
78	13	54.2	8472	9	US-09-764-868-1307	Sequence 1307, Ap
79	13	54.2	11177	10	US-09-764-878-231	Sequence 231, App
80	13	54.2	1587	10	US-09-764-877-2134	Sequence 2134, Ap
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82	13	54.2	31124	12	US-10-063-763-12	Sequence 12, Appl
83	13	54.2	31730	10	US-09-764-877-3510	Sequence 3510, Ap
84	13	54.2	127197	9	US-09-754-853A-1	Sequence 1, Appl1
85	13	54.2	203554	10	US-09-820-905-3	Sequence 3, Appl1
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87	12	50.0	148	10	US-09-960-332-5126	Sequence 5126, A
88	12	50.0	154	10	US-09-864-761-33750	Sequence 33750, A
89	12	50.0	171	10	US-09-983-965-2164	Sequence 2164, Ap
90	12	50.0	217	10	US-09-867-550-967	Sequence 967, App
91	12	50.0	249	10	US-09-563-817-84	Sequence 84, Appl
92	12	50.0	270	10	US-09-867-701-7646	Sequence 7646, Ap

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c 94 12 50.0 292 10 US-09-917-800A-1264
c 95 12 50.0 333 10 US-09-815-242-9155
c 96 12 50.0 340 10 US-09-880-107-862
c 97 12 50.0 343 10 US-09-764-869-272
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c 99 12 50.0 349 10 US-09-878-574-12
c 100 12 50.0 363 10 US-09-770-791-470

US-10-163-381-3
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Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 5 TCAAGGCTGTAATGA 19
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Db 10418 TCAAGGCTGTAATGA 10404

ALIGNMENTS

RESULT 1

US-09-738-878-3/c
; Sequence 3, Application US/09738878
; Patent No. US2002022254A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000744

; CURRENT APPLICATION NUMBER: US/09/738, 878

; CURRENT FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 30175

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(30175)

; OTHER INFORMATION: n = A,T,C or G

US-09-738-878-3

Query Match 62.5%; Score 15; DB 10; Length 30175;
Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 5 TCAAGGCTGTAATGA 19
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Db 10418 TCAAGGCTGTAATGA 10404

RESULT 2

US-10-163-381-3/c
; Sequence 3, Application US/10163381
; Patent No. US20020151015A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL000744CON

; CURRENT APPLICATION NUMBER: US/10/163,381

; CURRENT FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: 60/221,509

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/738, 878

; PRIOR FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 30175

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(30175)

; OTHER INFORMATION: n = A,T,C or G

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Run on: January 12, 2003, 10:48:53 ; Search time 19.1707 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-7

Sequence: 1 gtatgaagcgtgtaatgatcacc 24

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	62.5	12665	4	US-08-961-527-134	Sequence 134, App
C 4	58.3	225	4	US-09-134-001C-870	Sequence 870, App
C 5	58.3	834	2	US-08-967-101-113	Sequence 113, App
C 6	58.3	834	2	US-08-592-541-113	Sequence 113, App
C 7	58.3	834	3	US-09-124-698-113	Sequence 113, App
C 8	58.3	834	4	US-09-127-480-113	Sequence 113, App
C 9	58.3	834	4	US-08-496-841C-113	Sequence 113, App
C 10	58.3	834	4	US-09-124-523-113	Sequence 113, App
C 11	58.3	954	4	US-09-134-001C-875	Sequence 875, App
C 12	58.3	2417	4	US-09-605-785-334	Sequence 334, App
C 13	58.3	2417	4	US-09-439-313-334	Sequence 334, App
C 14	58.3	2417	4	US-09-352-616A-334	Sequence 334, App
C 15	58.3	2417	4	US-09-232-149A-334	Sequence 334, App
C 16	58.3	2560	4	US-08-961-527-114	Sequence 114, App
C 17	58.3	3674	4	US-09-605-785-698	Sequence 698, App
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C 19	58.3	56516	4	US-08-338-507-1	Sequence 1, Appli
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C 22	58.3	56520	4	US-09-218-207-179	Sequence 179, App
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C 27	54.2	227	4	US-08-991-789A-183	Sequence 183, App

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C 35	13	54.2	907	3	US-08-672-850-11	Sequence 11, Appli
C 36	13	54.2	908	4	US-09-457-046B-23	Sequence 23, Appli
C 37	13	54.2	1001	3	US-08-672-850-10	Sequence 10, Appli
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C 39	13	54.2	1210	2	US-08-483-695-4	Sequence 4, Appli
C 40	13	54.2	1210	2	US-07-865-285-4	Sequence 4, Appli
C 41	13	54.2	1210	2	US-08-487-231-4	Sequence 4, Appli
C 42	13	54.2	1210	2	US-09-201-912-4	Sequence 4, Appli
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C 45	13	54.2	1461	1	US-08-403-634-1	Sequence 1, Appli
C 46	13	54.2	1461	4	US-08-913-441B-1	Sequence 1, Appli
C 47	13	54.2	1555	4	US-09-509-902A-5	Sequence 5, Appli
C 48	13	54.2	1586	3	US-09-173-581-11	Sequence 11, Appli
C 49	13	54.2	1586	4	US-09-420-915-11	Sequence 11, Appli
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C 52	13	54.2	2141	4	US-09-441-039-1	Sequence 1, Appli
C 53	13	54.2	2142	4	US-09-441-039-3	Sequence 3, Appli
C 54	13	54.2	2526	3	US-08-669-408B-1	Sequence 1, Appli
C 55	13	54.2	2900	1	US-08-117-362-1	Sequence 1, Appli
C 56	13	54.2	2900	1	US-08-486-924-1	Sequence 1, Appli
C 57	13	54.2	2920	4	US-08-976-259-10	Sequence 10, Appli
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C 60	13	54.2	7780	4	US-08-961-527-18	Sequence 18, Appli
C 61	13	54.2	246240	2	US-08-724-394A-20	Sequence 20, Appli
C 62	13	54.2	246240	2	US-08-724-394A-21	Sequence 21, Appli
C 63	13	54.2	246240	2	US-08-724-394A-22	Sequence 22, Appli
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C 65	12	50.0	129	4	US-09-219-983A-15	Sequence 15, Appli
C 66	12	50.0	367	4	US-09-219-983A-13	Sequence 13, Appli
C 67	12	50.0	408	3	US-09-184-658-5	Sequence 5, Appli
C 68	12	50.0	573	4	US-09-328-111-221	Sequence 221, App
C 69	12	50.0	658	3	US-08-961-083-27	Sequence 27, Appli
C 70	12	50.0	739	1	US-07-872-678A-2	Sequence 2, Appli
C 71	12	50.0	883	3	US-09-184-658-7	Sequence 7, Appli
C 72	12	50.0	900	4	US-08-987-121A-1	Sequence 1, Appli
C 73	12	50.0	900	4	US-08-987-121A-2	Sequence 2, Appli
C 74	12	50.0	989	4	US-09-484-970B-149	Sequence 149, App
C 75	12	50.0	1006	3	US-08-961-083-51	Sequence 51, Appli
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C 79	12	50.0	1032	4	US-09-227-357-134	Sequence 134, App
C 80	12	50.0	1034	4	US-09-227-357-15	Sequence 15, Appli
C 81	12	50.0	1279	1	US-08-146-010A-4	Sequence 4, Appli
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C 83	12	50.0	1289	1	US-08-644-664B-13	Sequence 13, Appli
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C 85	12	50.0	1308	1	US-08-691-129-1	Sequence 1, Appli
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C 89	12	50.0	1340	3	US-09-184-658-8	Sequence 8, Appli
C 90	12	50.0	1364	2	US-08-872-302-3	Sequence 3, Appli
C 91	12	50.0	1410	3	US-08-668-392-1	Sequence 1, Appli
C 92	12	50.0	1410	3	US-08-396-988-1	Sequence 1, Appli
C 93	12	50.0	1410	4	US-08-886-634-1	Sequence 1, Appli
C 94	12	50.0	1426	4	US-09-349-851-1	Sequence 1, Appli
C 95	12	50.0	1426	2	US-08-303-569B-6	Sequence 6, Appli
C 96	12	50.0	1570	2	US-08-116-217-35	Sequence 35, Appli
C 97	12	50.0	1624	2	US-08-464-517-35	Sequence 35, Appli
C 98	12	50.0	1624	2	US-08-246-361A-35	Sequence 35, Appli
C 99	12	50.0	1624	3	US-08-463-772-35	Sequence 35, Appli
C 100	12	50.0	1624	5	PCT-US93-05000-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-858-207A-123/c
; Sequence 123, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Scodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-858-207A-123

Query Match 62.5%; Score 15; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 296 GTCGAAGGCTGTAATG 282
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RESULT 2
US-09-029-755C-1/c
; Sequence 1, Application US/09029755C
; Patent No. 6326477
; GENERAL INFORMATION:
; APPLICANT: ILMEN, Maxja
; APPLICANT: SOEDERLUND, Hans
; APPLICANT: PENTTILA, Metja
; TITLE OF INVENTION: PROCESS FOR MODIFYING GLUCOSE REPRESSION
; FILE REFERENCE: Substitute Sequence Listing-09-029755
; Patent No. 6326477
; CURRENT APPLICATION NUMBER: US/09/029,755C

; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: PCT/FI96/00463
; PRIOR FILING DATE: 1996-08-30
; PRIOR APPLICATION NUMBER: FI 954123
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2690
; TYPE: DNA
; ORGANISM: Trichoderma harzianum T3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (801)...(2027)
US-09-029-755C-1

Query Match 62.5%; Score 15; DB 4; Length 2690;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCTGTAATGATCATC 24
Db 1571 GCTGTAATGATCATC 1557
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RESULT 3

US-08-961-527-134
; Sequence 134, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-134

Query Match 62.5%; Score 15; DB 4; Length 12665;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GTCGAAGGCTGTAATG 18
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Title: US-09-424-705B-8

Perfect score: 32

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Scoring table: OLIGO_NTC
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23: em_pat:*
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25: em_pl:*
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27: em_sts:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_man:*
37: em_htg_vtl:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

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and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	19	59.4	29	6 AR043928	AR043928 Sequence
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6	19	59.4	29	6 AX022055	AX022055 Sequence
7	19	59.4	29	6 I93332	I93332 Sequence 2
8	19	59.4	30	6 AR165158	AR165158 Sequence
9	19	59.4	30	6 I06852	I06852 Sequence 9
10	19	59.4	33	6 AR021438	AR021438 Sequence
11	19	59.4	33	6 AR043000	AR043000 Sequence
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13	19	59.4	33	6 I62991	I62991 Sequence 11
14	19	59.4	33	6 I88744	I88744 Sequence 11
15	19	59.4	39	6 AR050899	AR050899 Sequence
16	19	59.4	41	6 A23167	A23167 Artificial
17	19	59.4	42	6 AR021399	AR021399 Sequence
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20	19	59.4	42	6 AX363263	AX363263 Sequence
21	19	59.4	42	6 I43947	I43947 Sequence 36
22	19	59.4	42	6 I62952	I62952 Sequence 47
23	19	59.4	42	6 I88705	I88705 Sequence 47
24	19	59.4	43	6 AR043942	AR043942 Sequence
25	19	59.4	43	6 AR073475	AR073475 Sequence
26	19	59.4	43	6 AX022069	AX022069 Sequence
27	19	59.4	43	6 I93346	I93346 Sequence 16
28	19	59.4	48	6 I03645	I03645 Sequence 6
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31	19	59.4	154	6 AR041047	AR041047 Sequence
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35	19	59.4	321	10 MMU294736	MMU294736
36	19	59.4	329	10 MMU5688	MMU5688 Mus musculus
37	19	59.4	330	10 AF276279	AF276279 Mus musculus
38	19	59.4	333	10 AF276285	AF276285 Mus musculus
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40	19	59.4	339	10 MNC581GKL	MNC581GKL
41	19	59.4	342	6 E40595	E40595
42	19	59.4	345	10 AF015483	AF015483
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46	19	59.4	345	10 MMU19004	MMU19004
47	19	59.4	345	10 AF420003	AF420003 Mus musculus
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56	19	59.4	348	10 MMU16070	MMU16070
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63	19	59.4	357	10 MUSIGLAB	MUSIGLAB
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Pred. No. is the number of results predicted by chance to have a

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C 95 19 59.4 363 10 MUSIGKAPB
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C 97 19 59.4 363 10 MUSL34IGKV
C 98 19 59.4 363 10 MUSL77IGKV
C 99 19 59.4 363 10 MUSL93IGKV
C 100 19 59.4 363 10 MMRNA240

ALIGNMENTS

RESULT 1
AR048860
LOCUS AR048860 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5824307.
ACCESSION AR048860
VERSION AR048860.1 GI:6004899
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,L.Sid.
TITLE Human-murine chimeric antibodies against respiratory syncytial virus
JOURNAL Patent: US 5824307-A 5 20-OCT-1998;
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source 1..24
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATGGATCCAGTTGGTGCGAGCATC 24

RESULT 2
I32409
LOCUS I32409 24 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 4 from patent US 5587458.
ACCESSION I32409
VERSION I32409.1 GI:1823200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS King,C.Richter.,Kasprzyk,P.G. and Bird,R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof
JOURNAL Patent: US 5587458-A 4 24-DEC-1996;
FEATURES Location/Qualifiers
source 1..24
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BASE COUNT 5 a 5 c 8 g 6 t
ORIGIN

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX060799 20 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 20 from patent WO0078815.
ACCESSION AX060799
VERSION AX060799.1 GI:12406179
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v?g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
JOURNAL Patent: WO 0078815-A 20 28-DEC-2000;
FEATURES Location/Qualifiers
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Db 2 CAGTTGGTGCGAGCATCAGC 20

RESULT 4
AR043928
LOCUS AR043928 29 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5817311.
ACCESSION AR043928
VERSION AR043928.1 GI:5965393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)
AUTHORS Bazin,H. and Latinne,D.
TITLE Methods of inhibiting T-cell mediated immune responses with

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 1024 Seconds
(without alignments)
506.109 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

Sequence: 1 ggggaagatgcatccagctgctgcagcagcagc 32

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

W size: 0
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

EST:
1: em_estbda:*
2: em_esthum:*
3: em_estinu:*
4: em_estnu:*
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13: gb_est4:*
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17: gb_gss:*
18: em_gss_hum:*
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26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	19	59.4	464	BM986668	BM986668 EST594262
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C 4	19	59.4	489	BI110707	BI110707 602896196
C 5	19	59.4	519	BM986669	BM986669 EST594263
C 6	19	59.4	532	BI104783	BI104783 602891329

C 7	19	59.4	537	14	BQ211527	BQ211527 UI-R-DV1-
C 8	19	59.4	540	10	AW917591	AW917591 EST348855
C 9	19	59.4	540	13	BG964740	BG964740 602899470
C 10	19	59.4	541	13	BM245196	BM245196 K0721C06-
C 11	19	59.4	541	9	AA819712	AA819712 UI-R-A0-a
C 12	19	59.4	553	10	BE309991	BE309991 601091717
C 13	19	59.4	553	13	BM194877	BM194877 L0702E09-
C 14	19	59.4	557	13	BM243211	BM243211 K0643C09-
C 15	19	59.4	569	12	BF580308	BF580308 602097044
C 16	19	59.4	569	13	BG964957	BG964957 602892924
C 17	19	59.4	575	13	BI249452	BI249452 602995789
C 18	19	59.4	577	10	BE305476	BE305476 601099542
C 19	19	59.4	585	13	BM194777	BM194777 L0700H12-
C 20	19	59.4	586	13	BM244148	BM244148 K0707C10-
C 21	19	59.4	594	10	BE309592	BE309592 601094848
C 22	19	59.4	594	14	BQ175706	BQ175706 UI-M-DJ2-
C 23	19	59.4	599	10	BE287315	BE287315 601093986
C 24	19	59.4	606	12	BF139980	BF139980 601791116
C 25	19	59.4	606	14	BQ222747	BQ222747 AGENCOURT
C 26	19	59.4	607	12	BF580281	BF580281 602097014
C 27	19	59.4	611	14	BQ175762	BQ175762 UI-M-DJ2-
C 28	19	59.4	620	10	BE368918	BE368918 601221562
C 29	19	59.4	624	10	BE306691	BE306691 601104076
C 30	19	59.4	626	12	BF582283	BF582283 602101109
C 31	19	59.4	630	12	BF138788	BF138788 601780387
C 32	19	59.4	631	13	BE284233	BE284233 UI-R-DA0-
C 33	19	59.4	638	10	BE284233	BE284233 601099177
C 34	19	59.4	639	12	BF583310	BF583310 602101781
C 35	19	59.4	641	12	BF134573	BF134573 601784982
C 36	19	59.4	643	12	BF579280	BF579280 602093454
C 37	19	59.4	659	12	BF137298	BF137298 601781658
C 38	19	59.4	660	13	BF113478	BF113478 602899340
C 39	19	59.4	669	12	BF123422	BF123422 601760623
C 40	19	59.4	671	13	BM194931	BM194931 L0703D04-
C 41	19	59.4	674	12	BF582339	BF582339 602101170
C 42	19	59.4	678	13	BF582341	BF582341 602827925
C 43	19	59.4	680	10	BE376043	BE376043 601229480
C 44	19	59.4	683	12	BF582936	BF582936 602101386
C 45	19	59.4	683	13	BI279213	BI279213 UI-R-DA0-
C 46	19	59.4	685	10	BE369854	BE369854 601212655
C 47	19	59.4	685	12	BG518843	BG518843 602578277
C 48	19	59.4	691	10	BE307937	BE307937 601096061
C 49	19	59.4	691	13	BI274417	BI274417 UI-R-CW0-
C 50	19	59.4	692	14	BQ198766	BQ198766 UI-R-EB0-
C 51	19	59.4	693	13	BG964281	BG964281 6028929076
C 52	19	59.4	693	13	BM171763	BM171763 imageGC.5
C 53	19	59.4	694	13	BG971707	BG971707 602858232
C 54	19	59.4	695	10	BE284224	BE284224 601099161
C 55	19	59.4	698	13	BI109045	BI109045 602896878
C 56	19	59.4	704	12	BF580765	BF580765 602093921
C 57	19	59.4	705	13	BG967208	BG967208 602833891
C 58	19	59.4	705	13	BI281292	BI281292 UI-R-DA0-
C 59	19	59.4	706	13	BG965094	BG965094 602829170
C 60	19	59.4	707	13	BI250555	BI250555 602993614
C 61	19	59.4	708	10	BE309445	BE309445 601095331
C 62	19	59.4	708	13	BI103114	BI103114 602889345
C 63	19	59.4	709	13	BG962745	BG962745 602830268
C 64	19	59.4	711	12	BF142976	BF142976 601791755
C 65	19	59.4	712	13	BI100311	BI100311 602885776
C 66	19	59.4	713	13	BI113389	BI113389 602900996
C 67	19	59.4	714	13	BG963548	BG963548 602891226
C 68	19	59.4	716	13	BG964192	BG964192 602828968
C 69	19	59.4	721	13	BG967689	BG967689 602833496
C 70	19	59.4	722	12	BF140170	BF140170 601786735
C 71	19	59.4	725	12	BF580940	BF580940 602100636
C 72	19	59.4	725	13	BG963055	BG963055 602828068
C 73	19	59.4	728	13	BG962985	BG962985 602827980
C 74	19	59.4	728	14	BQ139055	BQ139055 UI-R-EB0-
C 75	19	59.4	732	13	BG962768	BG962768 602830291
C 76	19	59.4	735	13	BG967206	BG967206 602833889
C 77	19	59.4	738	12	BF582153	BF582153 602099743
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C 85      19 59.4 754 14 BQ198977 UI-R-BAO-
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C 87      19 59.4 755 13 B1150509 602915167
C 88      19 59.4 762 12 BF144806 601791486
C 89      19 59.4 764 13 B1455283 603171949
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C 93      19 59.4 772 12 BF581992 602099448
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C 95      19 59.4 774 12 BF581989 602099444
C 96      19 59.4 774 12 BF123744 601760491
C 97      19 59.4 778 13 BG964076 602828830
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ALIGNMENTS

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LOCUS      BF139390      1063 bp      mRNA      linear      EST 24-OCT-2000
DEFINITION 601785258F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4013126 5',
            mRNA sequence.
ACCESSION  BF139390
VERSION     BF139390.1 GI:10978430
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 1063)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9255 row: c column: 15
            High quality sequence stop: 635.
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                /strain="CZECH II"
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                /lab_host="DH10B"
                /note="Organ: lung; Vector: pCMV-SPORT6; Site:1: NotI;
                Site 2: SalI; transgenic model WNT-1, expression driven by
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                dT. Library constructed by Life Technologies.
                Investigator providing samples: Gilbert Smith, NIH"
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ORIGIN

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LOCUS      BM986668      464 bp      mRNA      linear      EST 25-MAR-2002
DEFINITION  EST594262 Rat gene index, normalized rat, norvegicus Rattus
            norvegicus cDNA clone RGOAD95 3' end similar to anti-acetylcholine
            receptor antibody, mRNA sequence.
ACCESSION  BM986668
VERSION     BM986668
KEYWORDS   EST.
SOURCE     BM986668.1 GI:19706057
            Norway rat.
            Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 464)
            Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G.,
            Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.
            Generation of ESTs from a rat multiple tissue survey
            Unpublished (2001)
            Other ESTs: EST594263
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhleee@igrr.org
            This clone is available through the ATCC, contact the ATCC
            tel#703-365-2700 for further information
            Seq primer: M13 forward.
            Location/Qualifiers
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                /db_xref="taxon:10116"
                /clone="RGOAD95"
                /clone_lib="Rat gene index, normalized rat, norvegicus"
                /tissue_type="mixed tissue"
                /note="Vector: p7T3Pac; Site 1: EcoRI; Site 2: NotI;
                Combination of untreated and NGF-treated PC12 cell
                libraries, and Bento Soares normalized libraries of ovary,
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                muscle, spleen, heart"
BASE COUNT      102 a      112 c      121 g      129 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 10;
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DEFINITION  601089922F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3483797 5',
            mRNA sequence.
ACCESSION  BE289692
VERSION     BE289692
KEYWORDS   EST.
SOURCE     BE289692.1 GI:9170234
            house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 472)
            NIH-MGC http://mgc.nci.nih.gov/.
BASE COUNT      297 a      277 c      238 g      251 t
ORIGIN

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Query Match      62.5%; Score 20; DB 12; Length 1063;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 128.976 Seconds

(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

Sequence: 1 gggaaagatggatccagttgtgcagcaccagc 32

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wc size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_101002.*

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20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
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22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	75.0	24	AA116189	Anti-RSV F protein
2	75.0	24	AA165009	Anti-EBB2 antibody
3	59.4	20	AAV49835	LM609 grafted anti
4	59.4	20	AAV84782	HC and K antibody
5	59.4	20	AAH74638	PCR primer for lig
6	59.4	20	AA28190	Primer #2. Uniden
7	59.4	24	AA062720	Probe for detectio
8	59.4	24	AA062721	Probe for detectio
9	59.4	28	AAV45322	Kappa back primer.

10	19	59.4	28	AAV45318	FvK back primer.
11	19	59.4	29	AA071880	Lo-CD2a CL antisen
12	19	59.4	29	AAV62598	Lo-CD2a chimeric a
13	19	59.4	29	AAV22856	Lo-CD2a light chai
14	19	59.4	29	AAZ10123	Primer CL antisens
15	19	59.4	30	AAK35273	PCR primer used to
16	19	59.4	30	AAZ36147	PCR primer C-kappa
17	19	59.4	32	AAZ28085	Fusion gene huKS-m
18	19	59.4	32	AAZ30104	PCR primer used to
19	19	59.4	32	AAZ36145	PCR primer C-mu us
20	19	59.4	32	ABA99123	Sense primer #1 us
21	19	59.4	33	AAQ4196	PCR primer to ampl
22	19	59.4	33	AAZ37284	Mouse IgM light ch
23	19	59.4	33	AAV12579	Primer for mouse I
24	19	59.4	33	AAV73482	Mouse Igkappa cons
25	19	59.4	33	AAV38177	PCR primer for mou
26	19	59.4	33	AAZ21967	PCR primer used to
27	19	59.4	38	AAO53439	Sequence reverse C
28	19	59.4	39	AAV05548	S19 Mb kappa ligh
29	19	59.4	40	AAV09305	Murine anti-Protei
30	19	59.4	41	AAQ4387	Kappa II primer.
31	19	59.4	42	AAQ23440	Kappa light chain
32	19	59.4	42	AAQ4174	C-kappa light chai
33	19	59.4	42	AAZ12529	Probe specific for
34	19	59.4	42	AAV12529	Probe for mouse ka
35	19	59.4	42	AAV70512	Mouse Immunoglobul
36	19	59.4	42	AAV73463	Mouse kappa chain
37	19	59.4	42	AAV38146	Probe for the mous
38	19	59.4	42	AAZ21885	Probe used to isol
39	19	59.4	42	AAV06028	Mouse light chain
40	19	59.4	42	ABK43218	Recombinant adenov
41	19	59.4	43	AAV1893	Lo-CD2a VK PCR pri
42	19	59.4	43	AAV62612	Lo-CD2a chimeric a
43	19	59.4	43	AAZ2868	Lo-CD2a primer 3'
44	19	59.4	43	AAZ10137	PCR primer used to
45	19	59.4	44	AAQ78721	Primer to amplify
46	19	59.4	45	AAQ78720	Primer to amplify
47	19	59.4	145	AAZ22762	Partial scfVFL1-GF
48	19	59.4	318	AAZ28960	Mouse antibody 1C3
49	19	59.4	342	AAH27466	Murine coding sequ
50	19	59.4	349	AAV19521	Monoclonal antibod
51	19	59.4	354	AAI65596	Phosphonate ester
52	19	59.4	357	AAV1270	Anti-CEA antibody
53	19	59.4	358	AAQ5683	Sequence encoding
54	19	59.4	360	AAQ90434	DNA encoding anti-
55	19	59.4	360	AAV96344	cDNA for Ig light
56	19	59.4	360	AAZ39342	Rat anti-interleuk
57	19	59.4	363	AAQ37472	Sequence encoding
58	19	59.4	363	AAQ53992	LS2H241 light chai
59	19	59.4	363	AAQ56686	Sequence of the mo
60	19	59.4	363	AAO56688	Sequence of the mo
61	19	59.4	363	AAV38510	Light chain coding
62	19	59.4	363	AAV47893	Monoclonal antibod
63	19	59.4	363	AAV47895	MbD NP-01 light ch
64	19	59.4	363	AAV13951	Mouse j591 monoclo
65	19	59.4	363	AAV37832	j591 monoclonal an
66	19	59.4	363	AAZ65542	Murine monoclonal
67	19	59.4	364	AAV34816	Humanised anti-CD3
68	19	59.4	365	AAH41750	Monoclonal antibod
69	19	59.4	366	AAO27140	ICM-1 inhibiting
70	19	59.4	368	AAV05543	Nucleotide sequenc
71	19	59.4	368	AAV09793	DNA encoding the l
72	19	59.4	387	ABL5530	Anti-RANK ligand m
73	19	59.4	388	AAV66674	Anti-Fas MAb CH11
74	19	59.4	388	AAV78206	Anti-human Fas ant
75	19	59.4	391	AAV03378	Anti-IL-8 MAb 6G4.
76	19	59.4	391	AAV03224	Anti IL-8 antibody
77	19	59.4	391	AAV93547	Murine MAb (6G4.2.
78	19	59.4	391	AAV78588	Monoclonal antibod
79	19	59.4	391	AAV44949	Murine anti-IL-8 M
80	19	59.4	391	AAV10310	Murine monoclonal
81	19	59.4	391	AAV06415	Murine MAb (6G4.2.
82	19	59.4	391	AAV90571	Murine 6G4.2.5 mon

C 83 19 59.4 391 21 AAC65499 Murine 6G4-2-5 ant
 C 84 19 59.4 391 21 AAZ87960 Humanised 6G4.2.5
 C 85 19 59.4 396 22 AAH41752 Monoclonal antibod
 C 86 19 59.4 404 22 AAF81911 Anti-CA125 bifunct
 C 87 19 59.4 407 13 AAQ28254 VL FRP5. Mus musc
 C 88 19 59.4 407 21 AAZ49548 Mouse light chain
 C 89 19 59.4 418 17 AAT34152 Monoclonal antibod
 C 90 19 59.4 420 10 AAN90672 DNA sequence encod
 C 91 19 59.4 420 10 AAV60831 Variable light cha
 C 92 19 59.4 426 16 AAQ99848 Rat monoclonal ant
 C 93 19 59.4 426 22 AAD13177 Murine antibody ID
 C 94 19 59.4 429 18 AAT70811 Mouse anti-idiotyp
 C 95 19 59.4 432 12 AAQ15114 IL-2 chimeric anti
 C 96 19 59.4 435 12 AAQ15115 IL-2 chimeric anti
 C 97 19 59.4 435 14 AAQ36613 Anti-IL2R-alpha an
 C 98 19 59.4 435 18 AAT85149 Murine monoclonal
 C 99 19 59.4 435 20 AAV83772 Antibody 11D10 lig
 C 100 19 59.4 438 16 AAQ90431 DNA encoding anti-

ALIGNMENTS

RESULT 1

AAT16189
 ID AAT16189 standard; DNA; 24 BP.

AC AAT16189;
 DT 16-MAY-1996 (first entry)
 DE Anti-RSV F protein MAB 1129 VL PCR primer SJ11.

KW Humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB 1129; respiratory syncytial virus; RSV;
 KW light chain; complementarity determining region; CDR; primer; PCR;
 KW polymerase chain reaction; ss.

OS Synthetic.
 XX WO9605229-A1.

PN 22-FEB-1996.
 XX 09-AUG-1995; 95WO-US10053.

XX 15-AUG-1994; 94US-0290592.
 XX (MEDI-) MEDIMMUNE INC.

PA Johnson LS;
 PI WPI; 1996-139646/14.

DR New chimeric antibodies against respiratory syncytial virus -
 PT comprise human antibodies with CDR's from the variable heavy and
 PT light chains of a murine antibody
 XX Example 7; Page 18; 55pp; English.

CC Primers SJ42 (AAT16191) and SJ10 (AAT16188) were used to amplify
 CC cDNA from the murine monoclonal antibody (MAB) 1129 VH region.
 CC Primers SJ41 (AAT16190) and SJ11 (AAT16189) were similarly used to
 CC amplify the MAB 1129 VL region. MAB 1129 is active against
 CC respiratory syncytial virus (RSV) glycoprotein F antigenic site
 CC C. Mouse-human chimeric antibodies useful for treatment of RSV
 CC infection have been produced utilising the complementarity
 CC determining regions of the MAB 1129 VL and VH.

XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
 SQ Query Match 75.0%; Score 24; DB 17; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.0075;
 Mates 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 GATGATCCAGTTGGTGCAGCATC 29
 Db 1 GATGATCCAGTTGGTGCAGCATC 24

RESULT 2

AAT65009
 ID AAT65009 standard; DNA; 24 BP.

AC AAT65009;
 DT 05-JUN-1997 (first entry)

DE Anti-erbB2 antibody e23 light chain PCR primer.

KW Single chain antibody; variable region; light chain; heavy chain;
 KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
 KW immunodiagnosis; treatment; cytotoxic agent; erbB-2; ss.

OS Synthetic.
 XX US5587458-A.

PN 24-DEC-1996.
 XX 07-OCT-1991; 91US-0772270.

XX 14-MAY-1993; 93US-0061092.
 XX 07-OCT-1991; 91US-0772270.

XX 30-JUN-1992; 92US-0906555.
 XX (ARON-) ARONEX PHARM INC.

PA Bird RE, Kasprzyk PG, King CR;
 PI WPI; 1997-064831/06.

DR Single chain antibodies specific for erbB-2 protein, gp185 - with
 PT labels or cytotoxin, useful for detection and treatment of tumour
 PT cells expressing this protein
 XX Example 8; Column 18; 28pp; English.

CC Monoclonal antibody e23 was generated by immunising mice with
 CC N/erbB-2 cells overexpressing the gp185 protein, removing spleen
 CC cells and producing hybridomas by standard techniques. Messenger
 CC RNA coding for the anti-erbB-2 monoclonal antibody was isolated
 CC and converted to cDNA. Regions coding for the heavy- and light-
 CC chain variable regions were then amplified by PCR using primers
 CC having the sequences given in AAT65008-T65011 and joined via a
 CC sequence encoding a peptide linker. The resulting single-chain
 CC antibody, designated e23(FV), is useful for in vitro diagnosis of
 CC tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast,
 CC ovarian and non-small cell lung carcinomas, and, when coupled to a
 CC cytotoxic agent, to treat such tumours.

XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
 SQ Query Match 75.0%; Score 24; DB 18; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.0075;
 Mates 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GATGATCCAGTTGGTGCAGCATC 29
 Db 1 GATGATCCAGTTGGTGCAGCATC 24

RESULT 3

AAV49835
 ID AAV49835 standard; DNA; 20 BP.

AC AAV49835;
 DT 16-MAY-1996 (first entry)

DE Anti-RSV F protein MAB 1129 VL PCR primer SJ11.

KW Humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB 1129; respiratory syncytial virus; RSV;
 KW light chain; complementarity determining region; CDR; primer; PCR;
 KW polymerase chain reaction; ss.

OS Synthetic.
 XX WO9605229-A1.

PN 22-FEB-1996.
 XX 09-AUG-1995; 95WO-US10053.

XX 15-AUG-1994; 94US-0290592.
 XX (MEDI-) MEDIMMUNE INC.

PA Johnson LS;
 PI WPI; 1996-139646/14.

DR New chimeric antibodies against respiratory syncytial virus -
 PT comprise human antibodies with CDR's from the variable heavy and
 PT light chains of a murine antibody
 XX Example 7; Page 18; 55pp; English.

CC Primers SJ42 (AAT16191) and SJ10 (AAT16188) were used to amplify
 CC cDNA from the murine monoclonal antibody (MAB) 1129 VH region.
 CC Primers SJ41 (AAT16190) and SJ11 (AAT16189) were similarly used to
 CC amplify the MAB 1129 VL region. MAB 1129 is active against
 CC respiratory syncytial virus (RSV) glycoprotein F antigenic site
 CC C. Mouse-human chimeric antibodies useful for treatment of RSV
 CC infection have been produced utilising the complementarity
 CC determining regions of the MAB 1129 VL and VH.

XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
 SQ Query Match 75.0%; Score 24; DB 17; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.0075;
 Mates 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 24.9756 Seconds

(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705b-8

Perfect score: 32

Sequence: 1 ggggaagatgacccagtgtgcagcagcagc 32

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Wsize : 0
Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Published Applications NA:

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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
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14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	75.0	24	US-09-158-120A-5	Sequence 5, Appli
2	19	59.4	20	US-08-790-540A-20	Sequence 20, Appli
3	19	59.4	20	US-08-791-391A-20	Sequence 20, Appli
4	19	59.4	30	US-09-859-214-3	Sequence 3, Appli
5	19	59.4	357	US-09-910-059-8	Sequence 8, Appli
6	19	59.4	358	US-09-800-908-10	Sequence 10, Appli
7	19	59.4	360	US-09-905-243-65	Sequence 65, Appli
8	19	59.4	363	US-09-929-665-9	Sequence 9, Appli
9	19	59.4	363	US-09-929-665-10	Sequence 10, Appli
10	19	59.4	364	US-09-797-941A-3	Sequence 3, Appli
11	19	59.4	390	US-10-146-305-5	Sequence 5, Appli
12	19	59.4	407	US-09-924-099-27	Sequence 27, Appli
13	19	59.4	420	US-09-341-894-3	Sequence 95, Appli
14	19	59.4	426	US-09-840-459-95	Sequence 101, Appli
15	19	59.4	435	US-09-840-459-101	Sequence 1, Appli
16	19	59.4	435	US-09-861-294-1	Sequence 1, Appli
17	19	59.4	447	US-09-797-481-1	Sequence 3, Appli
18	19	59.4	447	US-09-844-736-3	Sequence 19, Appli
19	19	59.4	447	US-09-861-294-19	Sequence 19, Appli

C 20	19	59.4	447	10	US-09-990-205-1	Sequence 1, Appli
C 21	19	59.4	467	10	US-09-229-200A-5	Sequence 5, Appli
C 22	19	59.4	472	10	US-09-797-481-5	Sequence 5, Appli
C 23	19	59.4	504	12	US-10-006-773-14	Sequence 14, Appli
C 24	19	59.4	698	12	US-10-006-773-18	Sequence 18, Appli
C 25	19	59.4	729	12	US-10-006-773-10	Sequence 10, Appli
C 26	19	59.4	809	12	US-10-027-770-1	Sequence 1, Appli
C 27	19	59.4	831	9	US-09-903-327A-3	Sequence 3, Appli
C 28	19	59.4	1085	10	US-09-815-837-81	Sequence 81, Appli
C 29	19	59.4	1159	10	US-09-917-800A-1410	Sequence 1410, Ap
C 30	19	59.4	1161	10	US-09-917-800A-1401	Sequence 1401, Ap
C 31	19	59.4	1161	10	US-09-917-800A-1409	Sequence 1409, Ap
C 32	19	59.4	1161	10	US-09-917-800A-1411	Sequence 1411, Ap
C 33	19	59.4	1662	10	US-09-815-837-80	Sequence 80, Appli
C 34	19	59.4	1680	10	US-09-815-837-49	Sequence 49, Appli
C 35	19	59.4	1686	10	US-09-815-837-65	Sequence 65, Appli
C 36	19	59.4	1698	10	US-09-815-837-79	Sequence 79, Appli
C 37	19	59.4	5691	10	US-09-897-006-11	Sequence 11, Appli
C 38	19	59.4	5711	10	US-09-897-006-8	Sequence 8, Appli
C 39	19	59.4	6255	10	US-09-897-006-13	Sequence 13, Appli
C 40	18	56.2	293	10	US-09-867-701-5755	Sequence 5755, Ap
C 41	18	56.2	939	10	US-09-867-550-1621	Sequence 1621, Ap
C 42	16	50.0	30	10	US-09-855-271-4	Sequence 4, Appli
C 43	16	50.0	30	10	US-09-949-559-52	Sequence 52, Appli
C 44	16	50.0	38	9	US-09-991-470-19	Sequence 19, Appli
C 45	16	50.0	40	10	US-09-874-547-34	Sequence 34, Appli
C 46	16	50.0	354	10	US-09-949-559-105	Sequence 105, App
C 47	16	50.0	363	10	US-09-965-099-5	Sequence 5, Appli
C 48	16	50.0	363	12	US-10-051-852-5	Sequence 5, Appli
C 49	16	50.0	407	10	US-09-983-965-4802	Sequence 4802, Ap
C 50	15	46.9	39	10	US-09-859-214-63	Sequence 63, Appli
C 51	15	46.9	481	10	US-09-881-823-13	Sequence 13, Appli
C 52	15	46.9	1222	10	US-09-754-016-3	Sequence 3, Appli
C 53	15	46.9	1578	10	US-09-804-551B-35	Sequence 35, Appli
C 54	15	46.9	1934	10	US-09-754-016-1	Sequence 1, Appli
C 55	15	46.9	2519	10	US-09-917-800A-1647	Sequence 1647, Ap
C 56	15	46.9	4957	10	US-09-880-107-2154	Sequence 2154, Ap
C 57	14	43.8	16	10	US-09-158-120A-4	Sequence 4, Appli
C 58	14	43.8	34	10	US-09-782-874-8	Sequence 8, Appli
C 59	14	43.8	252	10	US-09-923-876-1845	Sequence 1845, Ap
C 60	14	43.8	309	10	US-09-954-456-196	Sequence 196, App
C 61	14	43.8	349	9	US-09-796-692-2634	Sequence 2634, Ap
C 62	14	43.8	370	10	US-09-880-107-804	Sequence 804, App
C 63	14	43.8	402	10	US-09-974-300-154	Sequence 154, App
C 64	14	43.8	460	9	US-10-046-935-73	Sequence 73, Appli
C 65	14	43.8	460	9	US-09-878-178-73	Sequence 73, Appli
C 66	14	43.8	637	10	US-09-770-119-635	Sequence 635, App
C 67	14	43.8	678	10	US-09-867-550-1347	Sequence 1347, Ap
C 68	14	43.8	770	10	US-09-910-943-27	Sequence 27, Appli
C 69	14	43.8	1110	9	US-10-041-006A-1	Sequence 1, Appli
C 70	14	43.8	1110	12	US-10-040-655-1	Sequence 1, Appli
C 71	14	43.8	1129	9	US-10-028-072-221	Sequence 221, App
C 72	14	43.8	1130	9	US-10-041-006A-8	Sequence 8, Appli
C 73	14	43.8	1130	12	US-10-040-655-8	Sequence 8, Appli
C 74	14	43.8	1241	10	US-09-764-855-205	Sequence 205, App
C 75	14	43.8	1241	8	US-08-881-509-1	Sequence 1, Appli
C 76	14	43.8	1386	10	US-09-823-830A-384	Sequence 384, App
C 77	14	43.8	1454	12	US-10-002-600-101	Sequence 101, App
C 78	14	43.8	1547	9	US-09-978-295A-465	Sequence 465, App
C 79	14	43.8	1547	9	US-09-978-192A-465	Sequence 465, App
C 80	14	43.8	1547	9	US-09-978-192A-465	Sequence 465, App
C 81	14	43.8	1547	9	US-09-999-832A-465	Sequence 465, App
C 82	14	43.8	1547	9	US-09-978-189-465	Sequence 465, App
C 83	14	43.8	1547	9	US-10-028-072-417	Sequence 417, App
C 84	14	43.8	1552	9	US-09-764-854-21	Sequence 21, Appli
C 85	14	43.8	1637	9	US-10-028-072-243	Sequence 243, App
C 86	14	43.8	1854	9	US-09-738-626-3076	Sequence 3076, Ap
C 87	14	43.8	1941	9	US-10-098-841-61	Sequence 61, Appli
C 88	14	43.8	2084	10	US-09-822-849A-267	Sequence 267, App
C 89	14	43.8	2233	9	US-09-764-857-13	Sequence 13, Appli
C 90	14	43.8	4148	10	US-09-350-874-54	Sequence 54, Appli
C 91	14	43.8	4253	9	US-10-098-841-205	Sequence 205, App
C 92	14	43.8				

C 93 14 43.8 5476 10 US-09-764-864-1790 Sequence 1790, Ap
 C 94 14 43.8 5476 10 US-09-764-864-1791 Sequence 1791, Ap
 C 95 14 43.8 5476 10 US-09-764-877-2811 Sequence 2811, Ap
 C 96 14 43.8 5476 10 US-09-764-877-2812 Sequence 2812, Ap
 C 97 14 43.8 5503 12 US-10-044-090-7 Sequence 7, Appl1
 C 98 14 43.8 6115 9 US-10-108-605-302 Sequence 302, App
 C 99 14 43.8 7107 10 US-09-070-927A-527 Sequence 527, App
 C 100 14 43.8 7430 10 US-09-956-004-64 Sequence 64, Appl

ALIGNMENTS

RESULT 1
 US-09-158-120A-5
 ; Sequence 5, Application US/09158120A
 ; Patent No. US20020102257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHNSON, L.
 ; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
 ; TITLE OF INVENTION: Respiratory Syncytial Virus
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; ADDRESSEE: STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: P160
 OPERATING SYSTEM: Windows95
 SOFTWARE: MS Word 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/158.120A
 FILING DATE: September 21, 1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/290.592
 FILING DATE: August 15, 1994
 APPLICATION NUMBER: 07/813.372
 FILING DATE: December 23, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Olstein, Elliot M.
 REGISTRATION NUMBER: 24,025
 REFERENCE/DOCKET NUMBER: 469201-367
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 973-994-1700
 TELEFAX: 973-994-1744

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 NUCLEOTIDES
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: Oligonucleotide
 US-09-158-120A-5

Query Match 75.0%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
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Qy 6 GATGGATCCAGTTGGTGACGATC 29
 Db 1 GATGGATCCAGTTGGTGACGATC 24

RESULT 2
 US-08-790-540A-20
 ; Sequence 20, Application US/08790540A
 ; Patent No. US2001001125A1

GENERAL INFORMATION:
 APPLICANT: Huse, William D.
 TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/790,540A
 FILING DATE: 30-JAN-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-IX 2405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-790-540A-20

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 Best Local Similarity 100.0%; Pred. No. 0.17;
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RESULT 3
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 ; Patent No. US20010016645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122

COMPUTER READABLE FORM:
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 COMPUTER: IBM PC compatible
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 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/791,391A
 FILING DATE: 30-JAN-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 25.561 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-8

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Scoring table: OLIGO_NTIC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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9	19	59.4	29	2	US-08-477-989B-2
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11	19	59.4	30	4	US-09-109-879-3
12	19	59.4	33	1	US-08-053-131-118
13	19	59.4	33	1	US-08-645-641-118
14	19	59.4	33	1	US-07-853-408B-118
15	19	59.4	33	1	US-08-096-762-118
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C 35	19	59.4	43	2	US-08-477-989B-16	Sequence 16, Appl
C 36	19	59.4	49	2	US-08-053-451B-151	Sequence 151, Appl
C 37	19	59.4	50	2	US-08-053-451B-152	Sequence 152, Appl
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C 39	19	59.4	154	2	US-08-053-451B-58	Sequence 58, Appl
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C 47	19	59.4	358	4	US-08-477-347-10	Sequence 10, Appl
C 48	19	59.4	360	1	US-08-318-970B-48	Sequence 48, Appl
C 49	19	59.4	360	1	US-08-447-422-13	Sequence 13, Appl
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C 88	19	59.4	420	6	US-08-653-402B-7	Sequence 7, Appl
C 89	19	59.4	435	4	US-09-096-244-1	Sequence 45, Appl
C 90	19	59.4	438	1	US-08-318-970B-45	Sequence 45, Appl
C 91	19	59.4	438	2	US-08-653-402B-11	Sequence 11, Appl
C 92	19	59.4	441	2	US-08-653-402B-3	Sequence 3, Appl
C 93	19	59.4	441	2	US-08-752-844-1	Sequence 1, Appl
C 94	19	59.4	447	2	US-08-579-940-1	Sequence 1, Appl
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C 96	19	59.4	447	4	US-08-838-693-1	Sequence 3, Appl
C 97	19	59.4	447	4	US-09-192-838B-1	Sequence 1, Appl
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Pred. No. is the number of results predicted by chance to have a

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C	16	1.1	34.4	121	6	AX263626	AX263626 Sequence
C	17	1.1	34.4	121	6	AX263627	AX263627 Sequence
C	18	1.1	34.4	121	6	AX263630	AX263630 Sequence
C	19	1.1	34.4	121	6	AX263631	AX263631 Sequence
C	20	1.1	34.4	121	6	AX263634	AX263634 Sequence
C	21	1.1	34.4	121	6	AX263635	AX263635 Sequence
C	22	1.1	34.4	125	11	AB059130	AB059130 Sus scrofa
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C	24	1.1	34.4	196	7	PMUBETAB	L24858 Human chrom
C	25	1.1	34.4	224	8	AY022862	M10194 Bacterioph
C	26	1.1	34.4	228	6	AX413071	AY022862 Oryza sat
C	27	1.1	34.4	228	6	AX415392	AX415392 Sequence
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C	31	1.1	34.4	236	4	PTSMTCOIA	W61135 Petriopus te
C	32	1.1	34.4	237	11	G03590	G03590 human STS W
C	33	1.1	34.4	249	10	MMU29443	U29443 Mus musculu
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C	40	1.1	34.4	260	10	MMU29375	U29375 Mus musculu
C	41	1.1	34.4	260	10	MMIKRPL96	X65007 M. musculu
C	42	1.1	34.4	260	10	MMIKRPL910	X65010 M. musculu
C	43	1.1	34.4	262	3	AF133855	AF133855 plasmidin
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ALIGNMENTS

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ACCESSION AX446316
VERSION AX446316.1 GI:21695215
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 2771 28-FEB-2002;
Illumina, Inc. (US)
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RESULT 2

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DEFINITION Synthetic Oligonucleotide I.
ACCESSION A07550
VERSION A07550.1 GI:413062
KEYWORDS
SOURCE synthetic construct.
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artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kaluza,B. and Lenz,H.
TITLE Diagnostic method using Chimeric antibodies
JOURNAL Patent: Ep 0378175-A 1 18-JUL-1990;
BOEHRINGER MANNHEIM GMBH
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VERSION AX203833.1 GI:15393278
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schall,T.J., Talbot,D., Miao,Z. and Wei,Z.
TITLE Tethered ligands and methods of use
JOURNAL Patent: WO 0146698-A 92 28-JUN-2001;
Chemocentryx, Inc. (US)
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DEFINITION Sequence 94 from Patent WO0146698.
ACCESSION AX203835
VERSION AX203835.1 GI:15393280
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 31)

```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 1024 Seconds
(without alignments)
506.109 Million cell updates/sec

Title: US-09-424-705b-9

Perfect score: 32

Sequence: 1 ggatgatactgctkctcaacycaatcccaagcaat 32

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Wd size: 0
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estrom:*
17: gb_ges:*
18: em_ges_hum:*
19: em_ges_inv:*
20: em_ges_pln:*
21: em_ges_vrt:*
22: em_ges_fun:*
23: em_ges_mam:*
24: em_ges_mus:*
25: em_ges_other:*
26: em_ges_pro:*
27: em_ges_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	34.4	41	14	H93873
2	11	34.4	51	17	BH789692
3	11	34.4	63	9	AA823595
4	11	34.4	71	14	N84974
5	11	34.4	73	10	BE095376
6	11	34.4	73	12	BF718854

7	11	34.4	82	10	AW705710
8	11	34.4	91	9	AA419631
9	11	34.4	99	14	BQ325678
10	11	34.4	99	17	AZ480278
11	11	34.4	100	14	BQ325755
12	11	34.4	103	10	BE364212
13	11	34.4	103	12	BF751283
14	11	34.4	104	14	BQ321957
15	11	34.4	104	17	AQ668984
16	11	34.4	105	12	BF836351
17	11	34.4	105	14	BQ332933
18	11	34.4	107	13	B3385948
19	11	34.4	109	9	AA411537
20	11	34.4	109	14	BQ372511
21	11	34.4	110	12	BF855916
22	11	34.4	110	14	BQ369451
23	11	34.4	112	10	BE344163
24	11	34.4	112	12	BF876064
25	11	34.4	114	10	BE092511
26	11	34.4	114	12	BF201228
27	11	34.4	115	12	BF744707
28	11	34.4	116	10	AW258431
29	11	34.4	118	2	HSW009505
30	11	34.4	119	9	AA414294
31	11	34.4	122	9	AA000451
32	11	34.4	122	14	BQ325955
33	11	34.4	124	9	AA659099
34	11	34.4	125	13	BM291719
35	11	34.4	125	14	BM813162
36	11	34.4	126	17	AL770446
37	11	34.4	127	14	BQ342991
38	11	34.4	127	14	H54266
39	11	34.4	128	12	BF177440
40	11	34.4	129	14	BQ321974
41	11	34.4	130	14	BQ342992
42	11	34.4	131	12	BF704824
43	11	34.4	132	12	BF925753
44	11	34.4	133	9	A1129630
45	11	34.4	133	10	AA482538
46	11	34.4	134	9	AL750929
47	11	34.4	134	12	BF827290
48	11	34.4	135	12	BF736126
49	11	34.4	136	9	AA499626
50	11	34.4	138	12	BF921285
51	11	34.4	138	14	N40482
52	11	34.4	139	12	BF955150
53	11	34.4	139	14	BQ369424
54	11	34.4	139	14	BQ369621
55	11	34.4	140	12	BF737758
56	11	34.4	142	9	AA490820
57	11	34.4	142	17	AL770445
58	11	34.4	143	13	B3313496
59	11	34.4	145	14	BQ310344
60	11	34.4	145	17	AL756927
61	11	34.4	146	10	AW737252
62	11	34.4	147	17	BH658418
63	11	34.4	149	17	BH194500
64	11	34.4	151	9	AV059045
65	11	34.4	151	12	BF740400
66	11	34.4	152	10	BE129921
67	11	34.4	152	12	BF920779
68	11	34.4	152	14	BQ310342
69	11	34.4	153	10	BE694046
70	11	34.4	153	14	BQ321924
71	11	34.4	156	14	BQ374332
72	11	34.4	157	13	BG565059
73	11	34.4	158	10	AA669447
74	11	34.4	159	13	B3313971
75	11	34.4	160	13	B1867243
76	11	34.4	160	14	BQ369623
77	11	34.4	161	13	BQ045450
78	11	34.4	162	9	AA247739
79	11	34.4	162	12	BF910950

AW705710 sk62904.Y
AA419631 VCS1F11.F
BQ325678 RCL-C1011
AZ480278 IM0301J12
BQ325755 RCL-C1011
BE364212 P11.12.C1
BF751283 RCL-BM642
BQ321957 MRO-CT054
AQ668984 LERJ1157F
BF836351 RCL-HT097
BQ332933 IL3-ET011
B3385948 BJ385948
AA411537 zv27h10.S
BQ372511 MRO-FN015
BF855916 PM2-FN021
BQ369451 RCL-GN007
BE344163 EST409325
BF876064 IL3-ET011
BE092511 IL2-BT073
BF201228 WHE0986_E
BF744707 QV2-BT061
AW258431 uq34h07.Y
A1044655 Homo sapi.
AA414294 v08h04.S
AA000451 me78d08.F
BQ325955 RCL-C1016
AA659099 nt99d09.S
BM291719 EST574261
BM813162 EST591255
AL770446 Arabidops
BQ342991 PMO-NN117
H54266 yq89g12.F1
BF177440 MYE5799.M
BQ321974 PMO-CT070
BQ342992 PMO-NN117
BF704824 FM1.52.A0
BF925753 IL3-NT022
A1129630 qc49d09.X
AA482538 45781.MAR
AL750929 AL750929
BF827290 CM4-HN002
BF736126 QV1-KT002
AA499626 v195h09.F
BF921285 PM2-NT016
N40482 yw74a12.F1
BF955150 PM2-NN022
BQ369424 RCL-GN007
BQ369621 RCL-GN003
BF737758 PMO-KT000
AA490820 aa49e07.S
AL770445 Arabidops
B3313496 dab88d09.F
BQ310344 MRO-BT450
AL756927 Arabidops
AW737252 EST338679
BH658418 BOMCM73TR
BH194500 TC3-13E10
AV059045 AV059045
BF740400 MRL-HB001
BE129921 945032G12
BF920779 MR2-NT013
BQ310342 MRO-BT450
BE694046 QV2-BT061
BQ321924 MRO-CT045
BQ374332 RCL-FT019
BG565059 CM4-CT065
AA669447 112822.MA
B3313971 dae80f10.F
B1867243 fte64d09.X
BQ369623 RCL-GN003
BQ045450 BT045450
AA247739 hte0056.S
BF910950 CM1-UT003

```

c 80      11 34.4 162 17 B76074
81      11 34.4 164 14 B0975655
82      11 34.4 165 9  AV059436
83      11 34.4 165 12 B855919
84      11 34.4 165 12 B624408
85      11 34.4 165 14 BQ310451
86      11 34.4 166 9  A1572747
87      11 34.4 166 14 BQ327161
88      11 34.4 167 9  AA284173
89      11 34.4 168 12 BF854470
90      11 34.4 168 14 BQ342862
91      11 34.4 169 9  AV060158
92      11 34.4 169 12 BF920277
93      11 34.4 169 14 D43538
94      11 34.4 171 12 BF823572
95      11 34.4 171 12 BF846944
96      11 34.4 171 14 BQ505576
97      11 34.4 172 9  AV142058
98      11 34.4 174 10 AW597658
99      11 34.4 174 12 BF287879
100     11 34.4 174 13 B1192240

```

ALIGNMENTS

```

RESULT 1
H93873
LOCUS
DEFINITION
YV08e06.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:242146 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR
(HUMAN);, mRNA sequence.
H93873
H93873.1 GI:1101169
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 41)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: M13RP1.

```

FEATURES

```

source
1..41
/organism="Homo sapiens"
/db_xref="GDB:3791279"
/db_xref="taxon:9606"
/clone="IMAGE:242146"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGATTAATTAAGATCTTTTITTTTTTTTTTTT 3'],

```

```

double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      7 a      15 c      9 g      10 t
ORIGIN
Query Match      34.4%; Score 11; DB 14; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 TCTCCAGCAAT 32
|||||
DB 26 TCTCCAGCAAT 36
|||||
RESULT 2
BH789692
LOCUS
DEFINITION
SALK_044478.47.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044478.47.05.x, DNA
sequence.
ACCESSION
BH789692
VERSION
BH789692.1 GI:19882790
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 51)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At1g01330.
Class: TDNA tagged.

```

FEATURES

```

source
1..51
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_044478.47.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      12 a      7 c      9 g      23 t
ORIGIN
Query Match      34.4%; Score 11; DB 17; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGATATCGT 11
|||||
DB 35 GGTGATATCGT 45
|||||

```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 128.976 Seconds
(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-9

Perfect score: 32

Sequence: 1 ggtgatctcgtkctcacycartccagcaat 32

Scoring table: OLIGO NUC
Gapox 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Mask size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: N_Geneseq_101002.*

1: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	32	21	AAA15021
2	23	71.9	33	21	AAK99179
3	23	71.9	33	21	ABK15810
4	11	34.4	24	22	ABD06712
5	11	34.4	24	24	ABO02764
6	11	34.4	24	24	ABO09419
7	11	34.4	24	24	ABO09460
8	11	34.4	30	21	AAA64461
9	11	34.4	40	21	AAZ43423

10	11	34.4	42	21	AAA50168	Antibody 5H7 light
11	11	34.4	47	13	AAQ27347	HindIII-SacI frag
12	11	34.4	47	22	AAK086569	Primer used to amp
13	11	34.4	50	22	AAK086573	Primer used to amp
14	11	34.4	60	24	ABN39364	Human spliced tran
15	11	34.4	65	24	ABN28639	Rat spliced trans
16	11	34.4	65	24	ABN53576	Mouse spliced tran
17	11	34.4	69	20	AAK05584	Anti-Staph (HAY) 9
18	11	34.4	71	24	AAD28222	TOP2 RNA used for
19	11	34.4	73	24	ABK09629	Human ovarian tuno
20	11	34.4	74	24	AAD28302	Alternative versio
21	11	34.4	97	22	ABK73158	Human foetal liver
22	11	34.4	97	22	AAK21593	Human brain expres
23	11	34.4	97	22	AAK47754	Human bone marrow
24	11	34.4	97	22	AAI53587	Probe #22273 used
25	11	34.4	109	24	ABL81083	Human ovarian can
26	11	34.4	118	22	ABK70641	Human foetal liver
27	11	34.4	118	22	ABK37201	Probe #15667 for g
28	11	34.4	118	22	AAK18887	Human brain expres
29	11	34.4	118	22	AAK44831	Human bone marrow
30	11	34.4	118	22	AAI25037	Probe #14970 for g
31	11	34.4	118	22	AAI50808	Probe #19494 used
32	11	34.4	118	24	ABK19070	Human genome-deriv
33	11	34.4	121	22	ABK78171	BRCA1 mutation cor
34	11	34.4	121	22	ABK78172	BRCA1 mutation cor
35	11	34.4	121	22	ABK78175	BRCA1 mutation cor
36	11	34.4	121	22	ABK78176	BRCA1 mutation cor
37	11	34.4	121	22	ABK78179	BRCA1 mutation cor
38	11	34.4	121	22	ABK78180	BRCA1 mutation cor
39	11	34.4	141	18	AAV75623	Staphylococcus aur
40	11	34.4	153	23	ABK27987	Drosophila melanog
41	11	34.4	153	23	AAK49766	Staphylococcus aur
42	11	34.4	153	23	AAK49789	Staphylococcus aur
43	11	34.4	153	23	AAK49910	Staphylococcus aur
44	11	34.4	153	23	AAK50727	Staphylococcus aur
45	11	34.4	167	21	AAK11825	Aspergillus niger
46	11	34.4	169	23	AAK50537	Staphylococcus aur
47	11	34.4	171	23	AAK50214	Staphylococcus aur
48	11	34.4	186	24	ABK76072	Corn tassal-derive
49	11	34.4	208	18	AAV75403	Staphylococcus aur
50	11	34.4	222	22	AAK14181	Human breast cance
51	11	34.4	228	24	AAK67749	Listeria innocua D
52	11	34.4	228	24	AAK69590	Listeria innocua D
53	11	34.4	238	22	AAH87964	Pepermint plant o
54	11	34.4	240	23	AAK48929	Staphylococcus aur
55	11	34.4	240	23	AAK48929	Staphylococcus aur
56	11	34.4	246	24	ABK17374	Human OREF polynuc
57	11	34.4	254	24	AAV77397	Human OREF polynuc
58	11	34.4	271	18	AAV77397	Staphylococcus aur
59	11	34.4	273	21	AAK06547	Human secreted pro
60	11	34.4	274	18	AAV78772	Staphylococcus aur
61	11	34.4	275	22	AAK23043	Human breast cance
62	11	34.4	276	24	ABK70942	Corn tassal-derive
63	11	34.4	277	16	AAK26692	Human gene signatu
64	11	34.4	280	24	ABK16705	Human OREF polynuc
65	11	34.4	281	22	ABK48302	Human breast cell
66	11	34.4	281	22	ABK66187	Human foetal liver
67	11	34.4	281	22	ABK33254	Probe #11720 for g
68	11	34.4	281	22	AAK14606	Human brain expres
69	11	34.4	281	22	AAK40350	Human bone marrow
70	11	34.4	281	22	AAI21107	Probe #11040 for g
71	11	34.4	281	22	AAI66372	Probe #15058 used
72	11	34.4	281	22	AAI06828	Probe #6819 used t
73	11	34.4	281	24	ABK14367	Human genome-deriv
74	11	34.4	296	24	ABK77887	Human OREF polynuc
75	11	34.4	296	24	ABK27242	Human secreted pro
76	11	34.4	298	21	AAK062729	Human genome-deriv
77	11	34.4	300	11	AAK06215	Monoclonal antibod
78	11	34.4	300	17	AAK63504	Monoclonal antibod
79	11	34.4	300	17	AAK36664	Human gene express
80	11	34.4	300	20	AAK21599	Human gene express
81	11	34.4	300	20	AAK21600	Human gene express
82	11	34.4	300	20	AAK21594	Human gene express

83 11 34.4 300 21 AAC03010 Human secreted pro
 84 11 34.4 302 20 AAX51691 Human secreted pro
 85 11 34.4 306 11 AAQ06228 VK domain of antib
 86 11 34.4 306 17 AAT63506 Monoclonal antibod
 87 11 34.4 306 17 AAT36660 Monoclonal antibod
 88 11 34.4 307 24 ABN20031 Human ORFX polynuc
 89 11 34.4 309 14 AAQ45948 Mab BW 2128 light
 90 11 34.4 315 22 AAL12887 Human breast cance
 91 11 34.4 315 22 AAL21758 Human breast cance
 92 11 34.4 315 24 ABN16562 Human ORFX polynuc
 93 11 34.4 316 21 AAC02853 Human secreted pro
 94 11 34.4 318 14 AAQ36942 VK fragment of ant
 95 11 34.4 318 17 AAT13271 Mucin-type synthe
 96 11 34.4 318 18 AAT79900 Anti-Factor IX Mab
 97 11 34.4 318 22 AAD21670 Humanised antibody
 98 11 34.4 318 22 AAF88095 H. pylori catalase
 99 11 34.4 318 22 AAF88152 H. pylori catalase
 100 11 34.4 318 24 ABK24005 Mouse-human light

ALIGNMENTS

RESULT 1
 AAA15021
 ID AAA15021 standard; DNA; 32 BP.
 CC
 XX AAA15021;
 AC
 DT 21-AUG-2000 (first entry)
 XX
 XX PCR primer used to amplify DNA encoding a murine kappa light chain.
 DE
 XX
 XX CD20-specific receptor; CD-20 specific redirected T cell; leukemia;
 KW CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;
 KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis;
 KW PCR primer; ss.
 XX
 OS Mus sp.
 XX
 XX WO200023573-A2.
 PN
 XX 27-APR-2000.
 PD
 XX
 XX 20-OCT-1999; 99WO-US24484.
 PF
 XX 20-OCT-1998; 98US-0105014.
 PR
 XX (CITY) CITY OF HOPE.
 PA
 XX Raubitschek A, Jensen MC, Wu AM;
 PI
 XX WPI; 2000-339676/29.
 DR
 XX
 XX Genetically engineered CD20-specific redirected T cells useful for
 PT treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+
 PT acute or chronic leukemia, and autoimmune disease .
 PS
 XX Example 1; Page 56; 58pp; English.
 CC PCR primers AAA15020-21 were used to amplify DNA encoding a murine
 CC kappa light chain. The amplified sequence was used to construct a
 CC synthetic CD20-specific chimeric receptor. The specification describes
 CC CD-20 specific redirected T cells which express and bear on the cell
 CC surface membrane a CD20-chimeric receptor comprising an intracellular
 CC signalling domain, a transmembrane domain and an extracellular domain,
 CC the extracellular domain comprising a CD20-specific receptor. The
 CC genetically engineered CD20-specific redirected T cells are useful
 CC for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or
 CC CD20+ acute or chronic leukemia, in a human patient having previously
 CC undergone myeloablative chemotherapy and stem cell rescue. The
 CC genetically engineered CD20-specific redirected T cells are also
 CC useful for abrogating an untoward B cell function, such as autoimmune

CC disease (lupus or rheumatoid arthritis) in a patient.
 XX
 SQ Sequence 32 BP; 7 A; 9 C; 5 G; 8 T; 3 other;
 Query Match 100.0%; Score 32; DB 21; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.1e-10;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GGTGATATCGTKCTCACYCARTCTCCAGCAAT 32
 Db 1 GGTGATATCGTKCTCACYCARTCTCCAGCAAT 32
 RESULT 2
 AAK99179
 ID AAK99179 standard; DNA; 33 BP.
 CC
 XX AAK99179;
 AC
 DT 12-JUN-2002 (first entry)
 XX
 XX 33-mer oligonucleotide #4 related to the invention.
 DE
 XX
 XX Mouse monoclonal antibody; murine; surface antigen pres1 epitope;
 KW hepatitis B virus; PCR; primer; ss.
 KW
 XX Unidentified.
 OS
 XX KR99008647-A.
 PN
 XX 05-FEB-1999.
 PD
 XX
 XX 02-JUL-1997; 97KR-0030694.
 PF
 XX
 XX 02-JUL-1997; 97KR-0030694.
 PR
 XX (KORE-) KOREA RES INST CHEM TECHNOLOGY.
 PA
 XX
 XX Hong HJ, Ryoo CJ;
 PI
 XX WPI; 2000-168375/15.
 DR
 XX
 XX Changeable region of mouse monoclonal antibody recognizing surface
 PT antigen pres1 epitope of hepatitis B virus and gene -
 PT
 XX Disclosure; Page 7; 14pp; Korean.
 PS
 XX The invention relates to a changeable region of mouse monoclonal antibody
 CC recognising surface antigen pres1 epitope of hepatitis B virus and gene.
 CC This polynucleotide sequence relates to a 33-mer oligonucleotide of the
 CC invention.
 CC
 SQ Sequence 33 BP; 8 A; 9 C; 5 G; 8 T; 3 other;
 Query Match 71.9%; Score 23; DB 21; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 10 GTKCTCACYCARTCTCCAGCAAT 32
 Db 11 GTKCTCACYCARTCTCCAGCAAT 33
 RESULT 3
 ABK15810
 ID ABK15810 standard; DNA; 33 BP.
 CC
 XX ABK15810;
 AC
 XX 20-MAY-2002 (first entry)
 DT
 XX Mouse monoclonal antibody associated oligonucleotide #4.
 DE
 XX

93 11 34.4 717 10 US-09-808-037-5 Sequence 5, Appli
94 11 34.4 720 10 US-09-976-787-30 Sequence 30, Appl
95 11 34.4 731 10 US-09-770-149-105 Sequence 105, Appl
c 96 11 34.4 797 9 US-10-002-344A-50 Sequence 50, Appl
97 11 34.4 797 10 US-09-764-864-1782 Sequence 1782, Ap
c 98 11 34.4 805 10 US-09-864-761-16986 Sequence 16986, A
c 99 11 34.4 807 12 US-10-062-254-307 Sequence 307, App
c 100 11 34.4 838 10 US-09-974-300-2052 Sequence 2052, Ap

ALIGNMENTS

RESULT 1
US-09-832-292-44/c
; Sequence 44, Application US/09832292
; Patent No. US20020177205A1
; GENERAL INFORMATION:
; APPLICANT: Rvazanov, Alexey
; TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: 601-1-098CIP
; CURRENT APPLICATION NUMBER: US/09/832,292
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 09/632,131
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-832-292-44

Query Match 34.4%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32
|||
Db 17 TCTCCAGCAAT 7

RESULT 2
US-09-864-864-166/c
; Sequence 166, Application US/09864864
; Patent No. US20020102679A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Secrist, Heather
; APPLICANT: Lodes, Michael J.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steve P.
; APPLICANT: Mannion, Jane
; APPLICANT: Benson, Darin R.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.523
; CURRENT APPLICATION NUMBER: US/09/864,864
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 166
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-864-166

Query Match 34.4%; Score 11; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32
|||
Db 35 TCTCCAGCAAT 25

RESULT 3

US-09-864-761-28949/c
; Sequence 28949, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES U
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28949
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022843.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.56

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(without alignments)
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Perfect score: 32

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

W-size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

- Issued Patents NA:*
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 - 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	34.4	24	US-08-855-910-46	Sequence 46, Appl
2	11	34.4	46	US-08-449-287-21	Sequence 21, Appl
3	11	34.4	47	US-08-449-287-22	Sequence 22, Appl
4	11	34.4	71	US-09-608-7308-10	Sequence 10, Appl
5	11	34.4	286	US-08-651-1558-18	Sequence 18, Appl
6	11	34.4	287	US-08-881-037-55	Sequence 55, Appl
7	11	34.4	300	US-08-308-494A-16	Sequence 16, Appl
8	11	34.4	300	US-08-308-494A-20	Sequence 20, Appl
9	11	34.4	302	US-08-557-309B-15	Sequence 15, Appl
10	11	34.4	309	US-08-457-393-3	Sequence 3, Appl
11	11	34.4	315	US-08-459-310-3	Sequence 3, Appl
12	11	34.4	318	US-08-783-853A-104	Sequence 104, Appl
13	11	34.4	318	US-09-344-050-104	Sequence 104, Appl
14	11	34.4	321	US-08-211-202-4	Sequence 4, Appl
15	11	34.4	321	US-08-783-853A-6	Sequence 6, Appl
16	11	34.4	321	US-09-344-050-6	Sequence 6, Appl
17	11	34.4	322	US-08-434-000A-11	Sequence 11, Appl
18	11	34.4	322	US-09-312-157-11	Sequence 11, Appl
19	11	34.4	324	US-08-483-749A-7	Sequence 7, Appl
20	11	34.4	324	US-08-881-037-56	Sequence 56, Appl
21	11	34.4	327	US-08-002-324-3	Sequence 3, Appl
22	11	34.4	327	PCT-US94-00261-3	Sequence 3, Appl
23	11	34.4	331	US-08-836-561-32	Sequence 32, Appl
24	11	34.4	335	US-08-783-853A-102	Sequence 102, Appl
25	11	34.4	335	US-09-344-050-102	Sequence 102, Appl
26	11	34.4	357	US-09-171-945-8	Sequence 8, Appl
27	11	34.4	379	US-08-145-617-5	Sequence 5, Appl

28	11	34.4	384	US-07-634-278-30	Sequence 30, Appl
29	11	34.4	384	US-08-477-728-30	Sequence 30, Appl
30	11	34.4	384	US-08-474-040-30	Sequence 30, Appl
31	11	34.4	384	US-08-487-200-30	Sequence 30, Appl
32	11	34.4	384	US-08-149-099C-6	Sequence 6, Appl
33	11	34.4	384	US-08-476-275-3	Sequence 3, Appl
34	11	34.4	384	US-08-656-586-1	Sequence 1, Appl
35	11	34.4	384	US-08-478-967A-6	Sequence 6, Appl
36	11	34.4	384	US-08-444-644-14	Sequence 14, Appl
37	11	34.4	384	US-08-484-537-30	Sequence 30, Appl
38	11	34.4	384	US-08-619-491-1	Sequence 1, Appl
39	11	34.4	384	US-08-232-246A-14	Sequence 14, Appl
40	11	34.4	384	US-08-475-815B-6	Sequence 6, Appl
41	11	34.4	384	PCT-US95-07302-1	Sequence 1, Appl
42	11	34.4	387	US-08-449-287-1	Sequence 1, Appl
43	11	34.4	390	US-08-659-567-1	Sequence 1, Appl
44	11	34.4	393	US-08-116-776B-39	Sequence 39, Appl
45	11	34.4	393	US-08-438-562-39	Sequence 39, Appl
46	11	34.4	393	US-08-483-528B-2	Sequence 2, Appl
47	11	34.4	393	US-08-673-799C-2	Sequence 2, Appl
48	11	34.4	393	US-09-393-385B-2	Sequence 2, Appl
49	11	34.4	405	US-09-134-001C-1672	Sequence 1672, Appl
50	11	34.4	434	US-08-480-784-34	Sequence 34, Appl
51	11	34.4	434	US-08-483-553-34	Sequence 34, Appl
52	11	34.4	434	US-08-487-002-34	Sequence 34, Appl
53	11	34.4	434	US-08-483-554B-34	Sequence 34, Appl
54	11	34.4	434	US-08-488-011B-34	Sequence 34, Appl
55	11	34.4	434	US-08-850-727-34	Sequence 34, Appl
56	11	34.4	434	PCT-US95-10202-34	Sequence 34, Appl
57	11	34.4	434	PCT-US95-10203-34	Sequence 34, Appl
58	11	34.4	434	PCT-US95-10220-34	Sequence 34, Appl
59	11	34.4	461	US-09-257-584-7	Sequence 7, Appl
60	11	34.4	462	US-07-946-421-25	Sequence 25, Appl
61	11	34.4	462	US-09-328-111-459	Sequence 459, Appl
62	11	34.4	555	US-08-479-089A-4	Sequence 4, Appl
63	11	34.4	636	US-09-328-111-226	Sequence 226, Appl
64	11	34.4	648	5455030-4	Patent No. 5455030
65	11	34.4	669	US-08-190-199A-66	Sequence 66, Appl
66	11	34.4	672	US-08-190-199A-62	Sequence 62, Appl
67	11	34.4	673	US-08-098-416-1141	Sequence 1141, Appl
68	11	34.4	677	US-09-221-017B-312	Sequence 312, Appl
69	11	34.4	705	US-09-171-945-16	Sequence 16, Appl
70	11	34.4	708	US-09-423-439-17	Sequence 17, Appl
71	11	34.4	711	US-08-190-199A-60	Sequence 60, Appl
72	11	34.4	711	US-08-061-092A-1	Sequence 1, Appl
73	11	34.4	711	US-08-190-199A-64	Sequence 64, Appl
74	11	34.4	711	US-08-468-252-4	Sequence 4, Appl
75	11	34.4	711	US-08-668-706B-4	Sequence 4, Appl
76	11	34.4	711	PCT-US95-10740-4	Sequence 4, Appl
77	11	34.4	717	US-09-142-974B-1	Sequence 1, Appl
78	11	34.4	719	US-08-279-772A-7	Sequence 7, Appl
79	11	34.4	720	US-08-061-092A-2	Sequence 2, Appl
80	11	34.4	720	US-08-802-486-10	Sequence 10, Appl
81	11	34.4	720	5455030-14	Patent No. 5455030
82	11	34.4	729	5455030-16	Patent No. 5455030
83	11	34.4	731	US-08-998-416-585	Sequence 585, Appl
84	11	34.4	732	US-08-553-497A-19	Sequence 19, Appl
85	11	34.4	732	US-08-860-882A-26	Sequence 26, Appl
86	11	34.4	732	US-09-423-439-57	Sequence 57, Appl
87	11	34.4	732	US-09-011-769A-22	Sequence 22, Appl
88	11	34.4	737	US-08-858-176A-183	Sequence 183, Appl
89	11	34.4	738	US-08-956-047-24	Sequence 24, Appl
90	11	34.4	738	5455030-6	Patent No. 5455030
91	11	34.4	751	US-07-985-694A-3	Sequence 3, Appl
92	11	34.4	752	5455030-12	Patent No. 5455030
93	11	34.4	758	US-08-279-772A-5	Sequence 5, Appl
94	11	34.4	759	US-08-902-486-8	Sequence 8, Appl
95	11	34.4	784	US-08-956-047-32	Sequence 32, Appl
96	11	34.4	786	US-08-635-928-31	Sequence 31, Appl
97	11	34.4	793	US-08-956-047-29	Sequence 29, Appl
98	11	34.4	810	US-08-652-507-1	Sequence 1, Appl
99	11	34.4	840	US-09-042-771-1	Sequence 1, Appl
100	11	34.4	843	US-09-423-439-43	Sequence 43, Appl

ALIGNMENTS

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RESULT 1
US-08-855-910-46
; Sequence 46, Application US/08855910
; Patent No. 6221640
; GENERAL INFORMATION:
; APPLICANT: Tao, Jianshi
; APPLICANT: Sassanfar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Avruch, Anthony S.
; APPLICANT: Yu, Russell V.
; APPLICANT: Nair, Shamila
; TITLE OF INVENTION: ENTEROCOCCAL AMINOACYL-tRNA SYNTHETASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,910
; FILING DATE: 14-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI95-08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-855-910-46
Query Match 34.4%; Score 11; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGATATCGT 11
Db 8 GGTGATATCGT 18

RESULT 2
US-08-449-287-21
; Sequence 21, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-449-287-21
Query Match 34.4%; Score 11; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32
Db 23 TCTCCAGCAAT 33

RESULT 3
US-08-449-287-22/c
; Sequence 22, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-449-287-21
Query Match 34.4%; Score 11; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32
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Title: US-09-424-705b-10

Perfect score: 38
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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41: em_hcgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	38	100.0	445	6 AX190429	AX190429 Sequence
3	32	84.2	38	6 AX083704	AX083704 Sequence
4	21	55.3	30	6 A44949	A44949 Sequence 5
5	21	55.3	30	6 I64440	I64440 Sequence 5
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7	21	55.3	383	10 AB062579	AB062579 Mus muscu
8	21	55.3	395	10 AB062569	AB062569 Mus muscu
9	21	55.3	395	10 AB062571	AB062571 Mus muscu
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19	21	55.3	398	10 AB062570	AB062570 Mus muscu
20	21	55.3	398	10 AB062573	AB062573 Mus muscu
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23	21	55.3	398	10 AB062592	AB062592 Mus muscu
24	21	55.3	401	10 AB062577	AB062577 Mus muscu
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29	21	55.3	404	10 AB062587	AB062587 Mus muscu
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31	21	55.3	405	10 AF113102	AF113102 Mus muscu
32	21	55.3	405	10 AF113103	AF113103 Mus muscu
33	21	55.3	411	6 AR085465	AR085465 Sequence
34	21	55.3	411	6 AR088871	AR088871 Sequence
35	21	55.3	411	6 I36728	I36728 Sequence 57
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ALIGNMENTS

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RESULT 1
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LOCUS
DEFINITION Sequence 4 from Patent WO9954440.
ACCESSION AX014265
VERSION AX014265.1 GI:10040640
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 39)
AUTHORS Bargou,R., Kufer,P., Loeffler,A. and Lutterbuese,R.
TITLE Cdl9xcd3 specific polypeptides and uses thereof
JOURNAL Patent: WO 9954440-A 4 28-OCT-1999;
RIETHMUELLER GERT (DE); BARGOU RALF (DE); DOERKEN BERND (DE); KUFER
PETER (DE); LOEFFLER ANJA (DE); LUTTERBUESE RALF (DE)
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/db_xref="taxon:32630"
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BASE COUNT 8 a 7 c 14 g 10 t
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Db 2 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGTCGTTTT 39
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LOCUS
DEFINITION Sequence 16 from Patent WO0147953.
ACCESSION AX190429
VERSION AX190429.1 GI:15143786
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 445)
AUTHORS Mueller-Hermelink,H.K., Greiner,A., Doerken,B., Bargou,R. and Kufer,P.
TITLE Antibodies against plasma cells
JOURNAL Patent: WO 0147953-A 16 05-JUL-2001;
Mueller-Hermelink, Hans Konrad (DE); Greiner, Axel (DE)
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AX083704 38 bp DNA linear PAT 28-FEB-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0111059.
ACCESSION AX083704
VERSION AX083704.1 GI:13185432
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Arndt,M., Little,M., Kyriyanov,S., Krauss,J. and Pfreundschuh,M.
TITLE F v? antibody construct comprising binding sites for a cd16
receptor and a cd30 surface protein
JOURNAL Patent: WO 0111059-A 5 15-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rech
(DE)
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A44949 30 bp DNA linear PAT 07-MAR-1997
LOCUS
DEFINITION Sequence 5 from Patent WO9515382.
ACCESSION A44949
VERSION A44949.1 GI:2299535

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 1216 Seconds
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Title: US-09-424-705B-10

Perfect score: 38

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

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Wo ze : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1097 row: f column: 06
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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ACCESSION  BB637724
VERSION    BB637724.1 GI:16473475
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 598.
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/clone_lib="NCI_CGAP_Lu29"
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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Qy      1 CCAGGGCCAGTGATAGACA 21
Db      501 CCAGGGCCAGTGATAGACA 481
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RESULT 2
B1149725/c
LOCUS      598 bp mRNA linear EST 05-JUL-2001
DEFINITION 602848572F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5012225 5',
mRNA sequence.
ACCESSION  B1149725
VERSION    B1149725.1 GI:14609726
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1062 row: p column: 18
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Stem cell origin."
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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BASE COUNT      140 a 165 c 151 g 142 t
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Best Local Similarity 100.0%; Pred. No. 0.12;
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Qy      1 CCAGGGCCAGTGATAGACA 21
Db      505 CCAGGGCCAGTGATAGACA 485
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LOCUS      632 bp mRNA linear EST 26-OCT-2001
DEFINITION BB637724 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530093J23 5', mRNA sequence.
ACCESSION  BB637724
VERSION    BB637724.1 GI:16473475
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1062 row: p column: 18
High quality sequence stop: 598.
Location/Qualifiers
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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BASE COUNT      140 a 165 c 151 g 142 t
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Qy      1 CCAGGGCCAGTGATAGACA 21
Db      505 CCAGGGCCAGTGATAGACA 485
      |||||
RESULT 3
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LOCUS      632 bp mRNA linear EST 26-OCT-2001
DEFINITION BB637724 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530093J23 5', mRNA sequence.
ACCESSION  BB637724
VERSION    BB637724.1 GI:16473475
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1062 row: p column: 18
High quality sequence stop: 598.
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/strain="CZECH II"
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Stem cell origin."
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
```



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XX Key Location/Qualifiers
FH misc_feature 256
FT /tag= a
FT /label= VH6
FT misc_feature 260..277
FT /tag= b
FT /label= DN1
FT misc_feature 281..323
FT /tag= c
FT /label= JH4
FT misc_feature 324..414
FT /tag= d
FT /label= m-gamma-1

XX WO9634096-A1.
XX 31-OCT-1996.
XX 28-APR-1995; 95WO-US05500.
XX 28-APR-1995; 95WO-US05500.
XX (CELL-) CELL GENESYS INC.
XX Brenner DG, Capon DJ, Jakobovits A, Klapholz S,
XX Kucherlapati R;
XX WPI: 1996-497628/49.
XX Antibody contg. fully human variable region specifically reactive
XX with antigen - prepd. by immunisation of non-human animal incapable
XX of producing endogenous immunoglobulin (Ig), but capable of
XX producing human Ig
XX Example 7; Fig 16; 64pp; English.
XX The present sequence encodes the heavy chain of the anti-tetanus
XX toxin (TT) human monoclonal antibody (Mab) K4.1, which was secreted
XX by the hybridoma K4.1 obtained by immortalising B cells from
XX xenomice (containing integrated human DNA from the immunoglobulin
XX locus) immunised with TT. The Mab can be used for analysis,
XX diagnosis, research and therapy, particularly for human therapeutic,
XX and in vivo diagnostic applications.
XX Sequence 414 BP; 98 A; 127 C; 98 G; 91 T; 0 other;
XX Query Match 55.3%; Score 21; DB 17; Length 414;
XX Best Local Similarity 100.0%; Pred. No. 0.089;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCAGGGGCCAGTGATAGACA 21
DB 364 CCAGGGGCCAGTGATAGACA 344

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PD 18-MAY-1999.
XX 29-OCT-1997; 97JP-0297451.
XX 29-OCT-1997; 97JP-0297451.
XX (NIHA ) JAPAN ENERGY CORP.
XX WPI: 1999-350322/30.
XX P-PSDB; AAY14355.
XX Neutralized antibody partial peptide derived from hepatitis C virus
XX - useful for inhibiting Hepatitis C Virus (HCV) serine protease
XX activity
XX Disclosure; Page 17-18; 32pp; Japanese.
XX This sequence represents the coding region for the heavy chain of the
XX anti-HCV Ser/Thr protease Mab 8D4. The invention relates to the use
XX of partial peptides (AAY14348-Y14353) from the Mab 8D4 for inhibiting
XX HCV serine protease activity.
XX Sequence 447 BP; 111 A; 115 C; 113 G; 108 T; 0 other;
XX Query Match 55.3%; Score 21; DB 20; Length 447;
XX Best Local Similarity 100.0%; Pred. No. 0.088;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCAGGGGCCAGTGATAGACA 21
DB 392 CCAGGGGCCAGTGATAGACA 372

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RESULT 6
AA57786/C
ID AA57786 standard: cDNA to mRNA; 447 BP.
XX AA57786;
XX 17-AUG-1999 (first entry)
XX Anti-HCV Ser/Thr protease Mab 8D4 heavy chain coding region.
XX Complementary determining region; CDR; monoclonal antibody; Mab;
XX hepatitis C virus; HCV; protease; ds.
XX Mammalia.
XX JP1127861-A.
XX

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```

RESULT 7
AAT59339/C
ID AAT59339 standard: cDNA; 486 BP.
XX AAT59339;
XX 21-AUG-1997 (first entry)
XX MH1 monoclonal antibody heavy chain encoding cDNA.
XX CDR; light chain; antigen binding site; antigen free animal;
XX germfree animal; immunoreactive; chromobiotic event; ss.
XX Mus musculus.
XX Key Location/Qualifiers
FH mat_peptide 1..486
FT /tag= a
FT /product= MH1_heavy_chain
FT misc_feature 82..96
FT /tag= b
FT /label= encodes_CDR1
FT misc_feature 139..189
FT /tag= c
FT /label= encodes_CDR2
FT misc_feature 286..321
FT /tag= d
FT /label= encodes_CDR3
XX WO9640986-A1.
XX 19-DEC-1996.
XX 29-APR-1996; 96WO-US07891.
XX 07-JUN-1995; 95US-0486420.
XX (AMBI-) AMERICAN BIOGENETIC SCI INC.
XX Dimitrijevic N, Dimitrijevic N;

```

CC chemotherapeutic agents. This sequence encodes the Wu-1 antibody,
CC variable region heavy chain fragment described in the method of the
CC invention.
XX
SQ Sequence 445 BP; 108 A; 109 C; 124 G; 104 T; 0 other;
Query Match 100.0%; Score 38; DB 22; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTTTT 38
DB 425 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTTTT 388
RESULT 3
AAF61154
ID AAF61154 standard; DNA; 38 BP.
XX
AC AAF61154;
XX
DT 18-MAY-2001 (first entry)
XX
DE Single chain Fv antibody construct A9 VH domain PCR primer VH3.
XX
KW Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
KW tumor cell; natural killer cell activation; Hodgkin's disease;
KW Reed-Sternberg disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN DE1937264-A1.
XX
PD 15-FEB-2001.
XX
PF 06-AUG-1999; 99DE-1037264.
XX
PR 06-AUG-1999; 99DE-1037264.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;
XX WPI; 2001-184000/19.
XX
DR New Fv-antibody construct, useful for treating Hodgkin and
PT Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30
PT surface protein
XX
PS Example 1; Page 11; 18pp; German.
XX
CC This invention describes a novel Fv-antibody construct (I) having binding
CC sites for a CD16 receptor and a CD30 surface protein. The invention also
CC describes (1) expression vector encoding (I); (2) transformants
CC containing the vector of (1); (3) preparation of (I) by culturing cells
CC of (2); and (4) kit comprising (I) and/or the vector of (1), and
CC auxiliaries such as buffers, solvents, carriers, controls and labels, or
CC their replacements. The products of the invention have cytostatic
CC activity. (I) causes lysis of CD30+, specifically tumor, cells. It
CC activates natural killer cells, through the CD16 receptor, and directs
CC them to CD30-expressing cells. (I) are used to treat diseases in which
CC CD30+ cells are implicated, particularly tumors and specifically Hodgkin
CC or Reed-Sternberg diseases. (I) have a stronger lytic action than known
CC bispecific antibodies, can be produced on a large scale with high purity,
CC and contain no components that can induce unwanted immune responses.
XX
SQ Sequence 38 BP; 7 A; 6 C; 14 G; 11 T; 0 other;
Query Match 84.2%; Score 32; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGT 32
DB 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGT 32
RESULT 4
AAx89880
ID AAX89880 standard; DNA; 30 BP.
XX
AC AAX89880;
XX
DT 18-OCT-1999 (first entry)
XX
DE Monoclonal antibody 8E5 Vh chain amplifying 3' primer.
XX
KW Fibrin; monoclonal antibody; MAb; 8E5; thrombosis; human;
KW thrombolytic disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CN1195701-A.
XX
PD 14-OCT-1998.
XX
PF 08-APR-1997; 97CN-0103756.
XX
PR 08-APR-1997; 97CN-0103756.
XX
PA (HEAM-) HEAMTOLOGY INST CHINESE ACAD SCI.
XX
PI Song Z;
XX
DR WPI; 1999-096572/09.
XX
PT Anti-human fibrin monoclonal antibody heavy chain and light chain
PT variable region gene - useful in thrombolytic medicine
XX
PS Example 2; Page 5; 16pp; Chinese.
XX
CC The invention provides a gene encoding light and heavy chain variable
CC regions of an anti-human fibrin monoclonal antibody (MAB). The gene is
CC used in the preparation of a diagnostic reagent for diagnosis of
CC thrombosis and in treatment of thrombolytic disorders. Sequences
CC AAX89879-80 represents PCR primers for amplifying the cDNA encoding the
CC Vh chain of MAb 8E5.
XX
SQ Sequence 30 BP; 5 A; 4 C; 11 G; 10 T; 0 other;
Query Match 71.1%; Score 27; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TGGATAGACAAAGCTTGGGTGCTTTT 38
DB 1 TGGATAGACAAAGCTTGGGTGCTTTT 27
RESULT 5
AAT38697/c
ID AAT38697 standard; cDNA; 414 BP.
XX
AC AAT38697;
XX
DT 01-JUL-1997 (first entry)
XX
DE Anti-tetanus toxin human monoclonal antibody K4.1 heavy chain cDNA.
XX
KW Heavy chain; tetanus; toxin; human; monoclonal; antibody; K4.1;
KW hybridoma; immortalisation; in vivo; xenomice; analysis;
KW immunoglobulin; diagnosis; research; therapy; B cell; ss.
XX
OS Homo sapiens.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 153.159 Seconds
(without alignments)
558,741 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38
Sequence: 1 ccaggggccagtgatagacaagcttggtgcgtttc 38

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	38	100.0	445	22	AAH21233
3	32	84.2	38	22	AAE61154
4	27	71.1	30	20	AA89880
5	21	55.3	414	17	AA738697
6	21	55.3	447	20	AAK57786
7	21	55.3	486	18	AA759339
8	21	55.3	531	12	AA015116
9	21	55.3	531	12	AA015117

10	21	55.3	615	15	AA062632
11	21	55.3	636	17	AA787815
12	21	55.3	642	20	AA228805
13	21	55.3	645	16	AA080293
14	21	55.3	666	15	AA073443
15	21	55.3	666	17	AA787817
16	21	55.3	699	22	AAH77315
17	21	55.3	717	16	AA092504
18	21	55.3	735	16	AA092500
19	21	55.3	777	17	AA742507
20	21	55.3	780	21	AA27848
21	21	55.3	798	13	AA030706
22	21	55.3	798	15	AA044642
23	21	55.3	830	13	AA030714
24	21	55.3	923	16	AA75136
25	21	55.3	1314	24	AA029310
26	21	55.3	1347	11	AA005708
27	21	55.3	1347	11	AA051334
28	21	55.3	1347	17	AA729056
29	21	55.3	1347	17	AA713733
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31	21	55.3	1392	19	AAV70129
32	21	55.3	1392	21	AA72108
33	21	55.3	1392	21	AAH1546
34	21	55.3	1392	24	ABL45925
35	21	55.3	1392	24	ABL48668
36	21	55.3	1392	24	AA597062
37	21	55.3	1443	15	AA062958
38	21	55.3	1446	18	AAV17340
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41	21	55.3	1528	5	AA040025
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67	21	55.3	1553	16	AA094037
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Porphyryn antibody
Antibody 7G12 heavy
Coding sequence fo
Monoclonal antibody
6D9 antibody heavy
Antibody 3G2 heavy
IgG Fab-BPI fusion
Mouse antibody H3-
Mouse antibody FB3
Murine ASB57 Fd fr
WOW-1 Fab heavy ch
Sequence of clone
Fd phage clone seq
Sequence of PCR pr
Murine Mab SK48-E2
Human penton base
Heavy chain of ant
Sequence encoding
Murine anti-BGH MA
Anti-BGH monoclon
Sequence encoding
Anti-Fas Mab HFE7A
cDNA encoding mous
Murine anti-Fas an
Mouse humanised an
Humanised anti-Fas
DNA encoding TPA-8
Glycophorin antio
Human B7.1-murine
Human penton base
Combined cDNA inse
mRNA encoding gamm
Anti-tobacco mosai
Mab 55.1 heavy cha
Murine anti-botuli
Murine anti-botuli
Murine anti-botuli
IAS MBP 1-14 CH1.H
IAS MBP 90-101 CH1
MBP 90-101 CH1
MBP 90-101 CH1.H.C
IAS MBP 1-14 CH1.C
Plasmd p10169 enc
Murine anti-botuli
Alpha-lactalbumin
Alpha-lactalbumin
Alpha-lactalbumin
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LMBOTC vector #1.
LMBOTC vector #1.
AD7 and 5C6 heavy
Gamma gene CH1 re
Murine gamma-1 gen
Anti-RSV F protein
Anti-erbA2 antibod
CHI immunoglobulin
Monoclonal antibod
IL-2 chimeric anti
Anti-IL2R-alpha an
Mouse monoclonal a
Light chain of an
Heavy chain of an
Recombinant 4G10 a
Sequence of mouse
IAS MBP 90-101 CH1
MBP 1-14 CH1.H.CHI

Sequence of mC-kap
Hepatitis B virus
Primer MCHC2. Syn
Immunoglobulin g1
PCR primer for the
PCR primer HA for
PCR primer J04 for
PCR primer J04 for
Surface-linked 4F1
SH7 scFv PCR prime
Anti-RANK ligand m
MURINE BSCA antio
Mouse heavy chain
VH186 region of an
Encodes murine ant
R6-5-D6 anti-ICAM-
Heavy chain of mon
Murine OKT4A heavy

83 19 50.0 19 13 AAQ25689
84 19 50.0 19 16 AAQ95067
85 19 50.0 23 13 AAQ28242
86 19 50.0 23 17 AAT29419
87 19 50.0 26 21 AAQ15025
88 19 50.0 28 12 AAQ15162
89 19 50.0 28 15 AAQ2767
90 19 50.0 28 15 AAQ2742
91 19 50.0 28 15 AAQ2742
92 19 50.0 89 24 AAD21982
93 19 50.0 97 21 ABL53531
94 19 50.0 399 22 AAF27975
95 19 50.0 453 22 AAF27975
96 19 50.0 453 24 ABK09984
97 19 50.0 458 12 AAQ15164
98 19 50.0 524 12 AAQ14802
99 19 50.0 524 12 AAQ14652
100 19 50.0 540 10 AAN91645
101 19 50.0 561 12 AAQ12630

ALIGNMENTS

RESULT 1
AAZ30327
ID AAZ30327 standard; DNA; 39 BP.
XX AC AAZ30327;
XX DT 11-FEB-2000 (first entry)
XX DE PCR primer 3'G used to amplify the variable heavy chain domain.
XX KW Variable heavy chain domain; HD37 hybridoma; bscCD19xCD3 antibody;
KW bispecific single-chain fragment; CD19 antigen; CD3 antigen;
KW CD19-positive target cell; T-cell stimulation; cytotoxic T-lymphocyte;
KW B-cell malignancy; B-cell mediated autoimmune disease; myasthenia gravis;
KW Morbus Basedow; Hashimoto thyroiditis; Goodpasture syndrome;
KW B-cell depletion; non-Hodgkin lymphoma; gene therapy; cancer;
KW viral disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO9954440-A1.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-EP02693.
XX PR 21-APR-1998; 98EP-0107269.
XX PA (DOERK) DOERKEN B.
XX PA (RIET) RIETHMUELLER G.
XX PI Kufer P, Lutterbues R, Bargou R, Loeffler A;
XX DR WPI; 2000-013241/01.
XX PT Novel multifunctional polypeptide for treating B-cell malignancies
XX PT especially non-Hodgkin lymphoma -
XX PS Example 1; Page 33; 91pp; English.
XX CC PCR primers AAZ30326-27 were used to amplify the variable heavy chain
CC domain from the HD37 hybridoma. The amplified sequence was cloned and
CC used to produce bispecific single-chain fragments, specifically a
CC bscCD19xCD3 antibody, comprising domains providing binding-site of
CC immunoglobulin chains or antibodies specifically recognizing CD19 and
CC CD3 antigen. The polypeptide destroys CD19-positive target cells without
CC any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic
CC T-lymphocytes and so specific lysis by T-cells rather than a direct
CC effect by an antibody is achieved. The bispecific single-chain
CC fragments, or nucleotides encoding them, are used for the treatment of

CC B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia
CC gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome
CC or for the depletion of B-cells and more particularly non-Hodgkin
CC lymphoma in mammals preferably human. They can also delay the
CC pathological conditions caused by these diseases, and can be used
CC for detecting these diseases. The polynucleotide is used for gene
CC therapy. The polypeptides are also used for identifying compounds
CC modulating B-cell/T-cell mediated immune response with can in turn be
CC used for treating cancer, its related diseases and also for inhibiting
CC viral diseases by preventing viral infection.
XX CC
XX Sequence 39 BP; 8 A; 7 C; 14 G; 10 T; 0 other;
Query Match 100.0%; Score 38; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGGGCCAGTCGATAGACAAAGCTTGGGTGCTGCTTTT 38
Db 2 CCAGGGCCAGTCGATAGACAAAGCTTGGGTGCTGCTTTT 39
RESULT 2
AAH21233/C
ID AAH21233 standard; DNA; 445 BP.
XX AC AAH21233;
XX DT 13-SEP-2001 (first entry)
XX DE Murine derived antibody Wue-1 variable region heavy chain DNA.
XX KW Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
KW immunomodulatory; cognate antigen identification; autoimmune disease;
XX tumor; multiple myeloma; lymphoma; plasmacytoma; ds.
XX OS Mus sp.
XX PN DE19962583-A1.
XX PD 28-JUN-2001.
XX PF 23-DEC-1999; 99DE-1062583.
XX PR 23-DEC-1999; 99DE-1062583.
XX PA (MUEL) MUELLER-HERMELINK H K.
XX PA (GREI) GREINER A.
XX PI Mueller-Hermelink HK, Greiner A;
XX DR WPI; 2001-426596/46.
XX PT New antibodies specific for plasma cells, useful for treatment and
XX PT diagnosis of autoimmune diseases and plasma cell tumors -
XX PS Claim 2; Page 13; 18pp; German.
XX CC This invention describes novel antibodies (Ab) in which the variable
CC region (VR) of at least one chain and/or the VR of at least one heavy
CC chain includes at least one of 7 specified sequences, or fragments of
CC these sequences, or contain at least one light chain and/or heavy
CC chain encoded by specific nucleic acid sequences (I) and (II),
CC reproduced, or their fragments. The products of the invention have
CC antitumor and immunomodulatory activity, Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursor stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 29.6585 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	21	55.3	1314	9 US-09-903-327A-5	Sequence 5, Appl
C 3	21	55.3	1446	10 US-09-910-059-130	Sequence 130, App
C 4	21	55.3	1516	9 US-09-903-327A-1	Sequence 1, Appl
C 5	21	55.3	1701	10 US-09-815-837-62	Sequence 62, Appl
C 6	21	55.3	1707	10 US-09-815-837-64	Sequence 64, Appl
C 7	21	55.3	1800	10 US-09-797-481-6	Sequence 67, Appl
C 8	21	55.3	2343	10 US-09-815-837-67	Sequence 61, Appl
C 9	21	55.3	2346	10 US-09-815-837-61	Sequence 61, Appl
C 10	21	55.3	5691	10 US-09-897-006-11	Sequence 11, Appl
C 11	21	55.3	5711	10 US-09-897-006-8	Sequence 8, Appl
C 12	21	55.3	6235	10 US-09-897-006-13	Sequence 13, Appl
C 13	20	52.6	27	10 US-09-158-120A-1	Sequence 1, Appl
C 14	20	52.6	761	12 US-10-006-773-16	Sequence 16, Appl
C 15	20	52.6	2053	10 US-09-815-837-63	Sequence 63, Appl
C 16	20	52.6	2059	10 US-09-815-837-66	Sequence 66, Appl
C 17	19	50.0	453	10 US-09-564-329A-14	Sequence 14, Appl
C 18	19	50.0	453	10 US-09-855-153-14	Sequence 14, Appl
C 19	19	50.0	453	10 US-09-854-811-14	Sequence 14, Appl

C 20	19	50.0	453	10 US-09-934-773-14	Sequence 14, Appl
C 21	19	50.0	453	10 US-09-963-620-14	Sequence 14, Appl
C 22	19	50.0	452	10 US-09-881-823-19	Sequence 19, Appl
C 23	19	50.0	561	10 US-09-229-200A-4	Sequence 4, Appl
C 24	19	50.0	682	12 US-10-006-773-8	Sequence 8, Appl
C 25	19	50.0	1013	10 US-09-815-837-85	Sequence 85, Appl
C 26	19	50.0	1676	10 US-09-815-837-82	Sequence 82, Appl
C 27	18	47.4	18	9 US-10-141-908-18	Sequence 18, Appl
C 28	17	44.7	28	9 US-09-423-800-3	Sequence 3, Appl
C 29	17	44.7	28	10 US-09-730-857-25	Sequence 25, Appl
C 30	17	44.7	28	10 US-09-924-099-26	Sequence 26, Appl
C 31	16	42.1	426	10 US-09-564-329A-12	Sequence 12, Appl
C 32	16	42.1	426	10 US-09-855-153-12	Sequence 12, Appl
C 33	16	42.1	426	10 US-09-854-811-12	Sequence 12, Appl
C 34	16	42.1	426	10 US-09-934-773-12	Sequence 12, Appl
C 35	16	42.1	426	10 US-09-963-620-12	Sequence 12, Appl
C 36	15	39.5	198285	10 US-09-880-107-3814	Sequence 3814, Ap
C 37	15	39.5	15	8 US-08-547-263-1	Sequence 1, Appl
C 38	15	39.5	15	10 US-09-229-200A-1	Sequence 1, Appl
C 39	15	39.5	15	10 US-09-158-120A-3	Sequence 3, Appl
C 40	15	39.5	15	10 US-09-962-436-202	Sequence 202, App
C 41	15	39.5	2000	9 US-09-938-842A-4789	Sequence 4789, Ap
C 42	15	39.5	2887	9 US-09-964-899-34	Sequence 34, Appl
C 43	15	39.5	2971	12 US-10-002-600-42	Sequence 42, Appl
C 44	15	39.5	92139	10 US-09-918-686-1	Sequence 1, Appl
C 45	15	39.5	167343	10 US-09-962-436-281	Sequence 281, App
C 46	15	39.5	167343	10 US-09-964-824A-273	Sequence 273, App
C 47	14	36.8	42	10 US-09-286-240-7	Sequence 7, Appl
C 48	14	36.8	173	10 US-09-880-107-80	Sequence 80, Appl
C 49	14	36.8	132	10 US-09-815-343-681	Sequence 681, App
C 50	14	36.8	132	10 US-09-815-343-1031	Sequence 1031, Ap
C 51	14	36.8	132	10 US-09-920-300A-739	Sequence 739, App
C 52	14	36.8	132	10 US-09-920-300A-944	Sequence 944, App
C 53	14	36.8	132	12 US-10-033-528-739	Sequence 739, App
C 54	14	36.8	132	12 US-10-033-528-944	Sequence 944, App
C 55	14	36.8	136	10 US-09-815-343-935	Sequence 935, App
C 56	14	36.8	409	10 US-09-864-761-16621	Sequence 16621, A
C 57	14	36.8	449	10 US-09-928-522-3	Sequence 3, Appl
C 58	14	36.8	451	10 US-09-864-761-5267	Sequence 5267, Ap
C 59	14	36.8	454	9 US-09-797-941-1	Sequence 1, Appl
C 60	14	36.8	454	9 US-09-933-797-189	Sequence 189, App
C 61	14	36.8	478	10 US-09-864-761-2335	Sequence 2335, Ap
C 62	14	36.8	518	10 US-09-881-823-17	Sequence 17, Appl
C 63	14	36.8	527	10 US-09-925-299-684	Sequence 684, App
C 64	14	36.8	527	10 US-09-925-299-684	Sequence 129, App
C 65	14	36.8	1244	9 US-10-002-344A-129	Sequence 101, App
C 66	14	36.8	1250	10 US-09-925-301-558	Sequence 538, App
C 67	14	36.8	1250	10 US-09-764-864-551	Sequence 551, App
C 68	14	36.8	1575	9 US-09-764-864-551	Sequence 9, Appl
C 69	14	36.8	1575	9 US-10-027-806-9	Sequence 9, Appl
C 70	14	36.8	1754	12 US-10-007-693-143	Sequence 143, App
C 71	14	36.8	1761	10 US-09-815-242-9838	Sequence 9838, Ap
C 72	14	36.8	1901	9 US-10-002-344A-130	Sequence 130, App
C 73	14	36.8	1946	10 US-09-925-299-242	Sequence 242, App
C 74	14	36.8	2078	12 US-10-044-091-175	Sequence 175, App
C 75	14	36.8	2167	9 US-10-028-072-159	Sequence 159, App
C 76	14	36.8	2269	9 US-09-860-298-1	Sequence 1, Appl
C 77	14	36.8	2848	9 US-10-002-344A-60	Sequence 60, Appl
C 78	14	36.8	5968	9 US-09-764-864-1501	Sequence 1501, Ap
C 79	14	36.8	10138	10 US-09-764-864-1046	Sequence 1046, Ap
C 80	14	36.8	23603	9 US-09-860-670-264	Sequence 264, App
C 81	14	36.8	23613	9 US-09-860-670-258	Sequence 258, App
C 82	14	36.8	24218	9 US-09-860-670-263	Sequence 263, App
C 83	14	36.8	32190	9 US-09-860-670-255	Sequence 255, App
C 84	14	36.8	32249	9 US-09-860-670-260	Sequence 260, App
C 85	14	36.8	42432	9 US-10-027-806-2	Sequence 2, Appl
C 86	14	36.8	42432	9 US-10-034-623-15	Sequence 15, Appl
C 87	13	34.2	30	10 US-09-813-659-15	Sequence 15, Appl
C 88	13	34.2	39	10 US-09-564-329A-26	Sequence 26, Appl
C 89	13	34.2	39	10 US-09-881-823-26	Sequence 26, Appl
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C 91	13	34.2	39	10 US-09-854-811-26	Sequence 26, Appl
C 92	13	34.2	39	10 US-09-934-773-26	Sequence 26, Appl

93 13 34.2 39 10 US-09-963-620-26 Sequence 26, Appl
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c 95 13 34.2 114 9 US-09-232-880-161 Sequence 161, App
c 96 13 34.2 114 9 US-10-012-896-161 Sequence 161, App
c 97 13 34.2 114 9 US-09-895-793-161 Sequence 161, App
c 98 13 34.2 114 9 US-09-895-814-161 Sequence 161, App
c 99 13 34.2 114 10 US-09-759-143-161 Sequence 161, App
c 100 13 34.2 114 10 US-09-780-669-161 Sequence 161, App

ALIGNMENTS

RESULT 1

US-10-006-773-12/c

; Sequence 12, Application US/10006773

; Patent No. US20020132983A1

; GENERAL INFORMATION:

; APPLICANT: Jungmans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti

; FILE REFERENCE: 003

; CURRENT APPLICATION NUMBER: US/10/006,773

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/250,089

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 736

; TYPE: DNA

; ORGANISM: Mus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (14)..(430)

; OTHER INFORMATION: 4D4 Heavy chain V region, plus leader

US-10-006-773-12

Query Match 55.3%; Score 21; DB 12; Length 736;

Best Local Similarity 100.0%; Pred. No. 0.0056;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21

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Db 471 CCAGGGCCAGTGGATAGACA 451

RESULT 2

US-09-903-327A-5/c

; Sequence 5, Application US/09903327A

; Patent No. US2002016433A1

; GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Erquang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1314

; TYPE: DNA

; ORGANISM: Mouse

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (0)..(1314)

; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein

; OTHER INFORMATION: bifunctional antibody

US-09-903-327A-5

Query Match 55.3%; Score 21; DB 9; Length 1314;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21

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Db 437 CCAGGGCCAGTGGATAGACA 417

RESULT 3

US-09-910-059-130/c

; Sequence 130, Application US/09910059

; Patent No. US20020142359A1

; GENERAL INFORMATION:

; APPLICANT: Copley, Clive G

; APPLICANT: Emery, Stephen Charles

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

; FILE REFERENCE: 1991-209

; CURRENT APPLICATION NUMBER: US/09/910,059

; CURRENT FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 09/171,945

; PRIOR FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: PCT/GB97/01165

; PRIOR FILING DATE: 1997-04-29

; PRIOR APPLICATION NUMBER: GB 9703103.3

; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7

; PRIOR FILING DATE: 1996-05-04

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 130

; LENGTH: 1446

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion

; NAME/KEY: CDS

; LOCATION: (16)..(1434)

; OTHER INFORMATION:

US-09-910-059-130

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1145 CCAGGGCCAGTGGATAGACA 1125

RESULT 4

US-09-903-327A-1/c

; Sequence 1, Application US/09903327A

; Patent No. US2002016433A1

; GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Erquang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1516

; TYPE: DNA

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 30.3537 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38
Sequence: 1 ccaagggccagctgacagacacgttcggtcgtttt 38

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C	21	55.3	411	2	US-08-331-397B-57	Sequence 57, Appl1	
C	21	55.3	411	2	US-08-759-804A-56	Sequence 56, Appl1	
C	5	21	55.3	636	2	US-08-737-129A-1	Sequence 1, Appl1
C	6	21	55.3	645	4	US-09-170-769A-5	Sequence 5, Appl1
C	7	21	55.3	666	2	US-08-737-129A-5	Sequence 5, Appl1
C	8	21	55.3	717	5	PCT-US94-14106-58	Sequence 58, Appl1
C	9	21	55.3	735	5	PCT-US94-14106-50	Sequence 50, Appl1
C	10	21	55.3	777	2	US-08-860-882A-25	Sequence 25, Appl1
C	11	21	55.3	777	4	US-09-011-769A-20	Sequence 20, Appl1
C	12	21	55.3	798	1	US-08-133-011-99	Sequence 99, Appl1
C	13	21	55.3	798	1	US-08-332-730A-99	Sequence 99, Appl1
C	14	21	55.3	798	1	US-08-387-874-71	Sequence 71, Appl1
C	15	21	55.3	798	1	US-08-383-619-99	Sequence 99, Appl1
C	16	21	55.3	798	4	US-08-907-739-99	Sequence 99, Appl1
C	17	21	55.3	798	4	US-09-729-597-99	Sequence 99, Appl1
C	18	21	55.3	798	5	PCT-US93-08364-71	Sequence 71, Appl1
C	19	21	55.3	830	1	US-08-133-011-115	Sequence 115, Appl1
C	20	21	55.3	830	1	US-08-332-730A-115	Sequence 115, Appl1
C	21	21	55.3	830	1	US-08-387-874-88	Sequence 88, Appl1
C	22	21	55.3	830	2	US-08-383-619-115	Sequence 115, Appl1
C	23	21	55.3	830	4	US-08-907-739-115	Sequence 115, Appl1
C	24	21	55.3	830	4	US-09-729-597-115	Sequence 115, Appl1
C	25	21	55.3	830	5	PCT-US93-08364-88	Sequence 88, Appl1
C	26	21	55.3	923	5	PCT-US94-07659-1	Sequence 1, Appl1
C	27	21	55.3	1347	6	5455030-2	Patent No. 5455030

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C	99	14	36.8	498	1	US-07-781-254A-14	Sequence 14, Appl1
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ALIGNMENTS

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; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/353.400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-353-400-5

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Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 57, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
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; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; OTHER INFORMATION: Heavy chain region"
US-08-331-398A-57

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; Sequence 57, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and U
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; SOFTWARE: Patent in Release #1.0, Version #1.30
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; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom

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SUMMARIES

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ALIGNMENTS

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ACCESSION      AX014264
VERSION        AX014264.1 GI:10040639
KEYWORDS
SOURCE          synthetic construct.
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 33)
AUTHORS      Bargon,R., Kufer,P., Loeffler,A. and Lutterbuesse,R.
TITLE        Cd19xcd3 specific polypeptides and uses thereof
JOURNAL      Patent: WO 9954440-A 3 28-OCT-1999;
            RIETHMUELLER GERT (DE); BARGOU RALF (DE); DOERKEN BERND (DE); KUFER
            PETER (DE); LOEFFLER ANJA (DE); LUTTERBUESE RALF (DE)
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LOCUS
DEFINITION      Synthetic construct single chain anti-transferrin receptor
                antibody-streptavidin fusion protein mRNA, complete cds.
ACCESSION      AF148718

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VERSION        AX011221.1 GI:9997801
KEYWORDS
SOURCE          synthetic construct.
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 33)
AUTHORS      Kipriyanov,S. and Little,M.
TITLE        Multivalent antibody constructs
JOURNAL      Patent: WO 9957150-A 16 11-NOV-1999;
            DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN
            (DE)
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ACCESSION      AX083703
VERSION        AX083703.1 GI:13185431
KEYWORDS
SOURCE          synthetic construct.
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 35)
AUTHORS      Arndt,M., Little,M., Kypriyanov,S., Krauss,J. and Pfreundschuh,M.
TITLE        F v? antibody construct comprising binding sites for a cd16
                receptor and a cd30 surface protein
JOURNAL      Patent: WO 0111059-A 4 15-FEB-2001;
            Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rech
            (DE)
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LOCUS
DEFINITION      Synthetic construct single chain anti-transferrin receptor
                antibody-streptavidin fusion protein mRNA, complete cds.
ACCESSION      AF148718

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ALIGNMENTS

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RESULT 1
BB564459/c 290 bp mRNA linear EST 29-NOV-2000
LOCUS BB564459 RIKEN full-length enriched, adult male small intestine Mus
DEFINITION musculus CDNA clone 2010014G07 5', mRNA sequence.
ACCESSION BB564459
VERSION BB564459.1 GI:11455351
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

```

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REFERENCE
AUTHORS Hanagaki, T., Hayashi, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, D., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sakai, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Taya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

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Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermolabile and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitanai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for

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further details. Location/Qualifiers
1..290
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="2010014G07"
/clone_lib="RIKEN full-length enriched, adult male small intestine"
/sex="male"
/tissue type="small intestine"
/dev stage="adult"
/lab host="SOLR"
/notes="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGGCCCACTCGAGTGTGTTTATTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGCGGCCCACTCGAGTGTGTTTATTTTNN 3']. cDNA was cleaved with XhoI and SstI."
BASE COUNT 82 a 79 c 84 g 45 t
ORIGIN

```

```

Query Match 42.1%; Score 16; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CGGCCATGGCGCAGGT 20
|||
Db 114 CGGCCATGGCGCAGGT 99
|||

```

```

RESULT 2
BF226545/c 348 bp mRNA linear EST 29-DEC-2000
LOCUS BF226545 NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:3672445 5'
DEFINITION similar to TR:Q922P7 Q922P7 GES30. i, mRNA sequence.
ACCESSION BF226545
VERSION BF226545.1 GI:11134311
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

```

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
MG1:1433213
High quality sequence stop: 297.
Location/Qualifiers
1..348
/organism="Mus musculus"
/db_xref="taxon:10090"

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 153.159 Seconds
(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-11

Perfect score: 38
Sequence: 1 cagccgcgcattggcgcaggtctcagctcagcagagtcwsg 38

Scoring table: OLIGO_NUC
Gapox 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Mo ze : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	86.8	33	21	AAZ30336
2	23	60.5	32	21	AAK99182
3	23	60.5	32	21	ABK15813
4	22	57.9	22	21	AAAI5024
5	20	52.6	33	21	AAZ43426
6	20	52.6	35	22	AA611153
7	20	52.6	898	19	AAV73335
8	20	52.6	1653	21	AAZ43432
9	20	52.6	1698	21	AAZ43431

10	20	52.6	1794	19	AAV73337	Mouse bispecific a
11	18	47.4	2031	21	AAA13527	Phagemid ph7 gene
12	17	44.7	56	22	AAH25553	Primer used to amp
13	17	44.7	348	13	AAQ22736	RSV9 VH. Mus mus
14	17	44.7	348	14	AAQ49376	RSV9 heavy chain
15	17	44.7	445	22	AAH21233	Murine derived ant
16	16	42.1	22	21	AAAI5023	PCR primer VHB13c
17	16	42.1	348	24	ABN19080	Human ORFX polyom
18	16	42.1	684	22	ABD01494	Murine apoptosis r
19	16	42.1	1350	24	AAO03282	Aspergillus niger
20	16	42.1	1449	22	AAO03286	Carrot extensin le
21	16	42.1	1515	18	AAQ96709	Aspergillus niger
22	16	42.1	2363	15	AAQ58126	Phyase gene. Asp
23	16	42.1	2379	15	AAQ56944	A. niger phytase g
24	15	39.5	34	18	AAQ62576	1.1ASML VHBAC o1
25	15	39.5	35	18	AAQ61508	Primer HUVH2.NCO f
26	15	39.5	38	24	AAQ98444	Human V gene 1ibra
27	15	39.5	38	24	AAQ98445	Human V gene 1ibra
28	15	39.5	38	24	AAQ98447	Human V gene 1ibra
29	15	39.5	38	24	AAQ98449	Human V gene 1ibra
30	15	39.5	39	24	ABA95762	Murine metallochio
31	15	39.5	60	13	AAQ32261	General Pab PCR pr
32	15	39.5	969	22	AAQ30730	Antibody 8860 biva
33	15	39.5	978	22	AAQ30728	Anti-FIX/Fix anti
34	15	39.5	993	21	AAAI3528	Phagemid ph17 fusi
35	15	39.5	1100	21	AAQ44049	Zea mays DNA fragm
36	15	39.5	1173	18	AAQ61867	Mouse ATP sensitiv
37	15	39.5	1173	21	AAQ39799	DNA sequence of mo
38	15	39.5	1332	18	AAQ67087	Mouse k-ATP channe
39	15	39.5	1352	19	AAV53711	Mouse ATP-sensitiv
40	15	39.5	2199	22	AAQ30727	Anti-FIX/Fix anti
41	15	39.5	4570	22	AAQ61152	Single chain Fv an
42	15	39.5	17091	20	AAQ60096	Acetobacter xylinu
43	14	36.8	20	18	AAQ61192	Primer VH2 for hea
44	14	36.8	20	19	AAV18687	Human immunoglobul
45	14	36.8	21	21	AAQ58680	Primer VHBAC. S
46	14	36.8	21	21	AAZ43496	Human antibody hea
47	14	36.8	21	21	AAZ43498	Human antibody hea
48	14	36.8	21	21	AAQ23475	PCR primer VHBAC
49	14	36.8	22	13	AAQ23579	VHBAC PCR primer
50	14	36.8	22	13	AAQ26701	Fusion antibody pr
51	14	36.8	22	13	AAQ27170	Primer VHBAC. S
52	14	36.8	22	13	AAQ28244	Primer VHBAC. S
53	14	36.8	22	13	AAQ28244	PCR primer VHBAC
54	14	36.8	22	13	AAQ30564	PCR primer VH01 f
55	14	36.8	22	13	AAQ32770	Primer VH01. Syn
56	14	36.8	22	14	AAQ34933	VH chain cDNA PCR
57	14	36.8	22	14	AAQ36936	PCR primer VHBAC
58	14	36.8	22	14	AAQ49620	PCR primer for amp
59	14	36.8	22	15	AAQ62522	Primer used in con
60	14	36.8	22	15	AAQ56749	Primer VHBAC.
61	14	36.8	22	15	AAQ65380	muMbd495 heavy cha
62	14	36.8	22	15	AAQ62768	PCR primer VHBAC
63	14	36.8	22	15	AAQ62743	PCR primer VHBAC
64	14	36.8	22	15	AAQ69188	HP1/2 PCR primer V
65	14	36.8	22	15	AAQ67353	Heavy chain PCR pr
66	14	36.8	22	15	AAQ45249	Mouse anti-KLH VH
67	14	36.8	22	15	AAQ78787	Primer VHBAC bas
68	14	36.8	22	16	AAQ74652	Mouse derived VH R
69	14	36.8	22	16	AAQ75039	Ig heavy chain vari
70	14	36.8	22	16	AAQ75023	Heavy chain variab
71	14	36.8	22	16	AAQ75003	Murine VH conserve
72	14	36.8	22	16	AAQ75026	Primer VHBAC for
73	14	36.8	22	16	AAQ82812	Antisense PCR prim
74	14	36.8	22	16	AAQ76283	OMV10 heavy chain
75	14	36.8	22	16	AAQ91376	PCR primer VHBAC
76	14	36.8	22	17	AAQ36591	Murine antibody 58
77	14	36.8	22	17	AAQ45077	Primer VHBAC, am
78	14	36.8	22	17	AAQ42048	Mouse heavy chain
79	14	36.8	22	17	AAQ29144	Primer VHBAC for
80	14	36.8	22	17	AAQ26854	Murine monoclonal
81	14	36.8	22	17	AAQ29016	Primer VHBAC for
82	14	36.8	22	17	AAQ29421	Immunoglobulin con

83 VH1BACK primer for
84 Primer for amplify
85 Primer VH1BACK for
86 Construction of tr
87 Primer RVH-1BACK f
88 Murine MAB B7 heav
89 RT-PCR primer VH1B
90 PCR primer, VH1BAC
91 Primer PCR.51 used
92 PCR primer for hea
93 Human sialic acid
94 PCR primer 1. Syn
95 MAB FC-2.15 V regi
96 Ing of pluck2001 P
97 Monoclonal antibod
98 PCR primer for lla
99 Llama antibody hea
100 Llama HC-V domain

ALIGNMENTS

RESULT 1
AAZ30326
ID AAZ30326 standard; DNA; 33 BP.

XX AAZ30326;
XX
DT 11-FEB-2000 (first entry)

XX PCR primer 5'H1 used to amplify the variable heavy chain domain.
XX
XX Variable heavy chain domain; HD37 hybridoma; bscCD19xCD3 antibody;
KW bispecific single-chain fragment; CD19 antigen; CD3 antigen;
KW CD19-positive target cell; T-cell stimulation; cytotoxic T-lymphocyte;
KW B-cell malignancy; B-cell mediated autoimmune disease; myasthenia gravis;
KW Morbus Basedow; Hashimoto thyroiditis; Goodpasture syndrome;
KW B-cell depletion; non-Hodgkin lymphoma; gene therapy; cancer;
KW viral disease; PCR primer; ss.

XX Synthetic.
XX
XX WO9954440-A1.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-EP02693.
XX
XX 21-APR-1998; 98EP-0107269.
XX
XX (DOER/) DOERKEN B.
XX (RIET/) RIETHMUELLER G.
XX
XX Kufer P, Lutterbuese R, Bargou R, Loeffler A;
XX
XX WPI; 2000-013241/01.

XX Novel multifunctional polypeptide for treating B-cell malignancies
PT especially non-Hodgkin lymphoma -
XX
XX Example 1; Page 33; 91pp; English.

XX PCR primers AAZ30326-27 were used to amplify the variable heavy chain
XX domain from the HD37 hybridoma. The amplified sequence was cloned and
XX used to produce bispecific single-chain fragments, specifically a
XX bscCD19xCD3 antibody, comprising domains providing binding-site of
XX immunoglobulin chains or antibodies specifically recognizing CD19 and
XX CD3 antigen. The polypeptide destroys CD19-positive target cells without
XX any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic
XX T-lymphocytes and so specific lysis by T-cells rather than a direct
XX effect by an antibody is achieved. The bispecific single-chain
XX fragments, or nucleotides encoding them, are used for the treatment of

CC B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia
CC gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome
CC or for the depletion of B- cells and more particularly non-Hodgkin
CC lymphoma in mammals preferably human. They can also delay the
CC pathological conditions caused by these diseases, and can be used
CC for detecting these diseases. The polynucleotide is used for gene
CC therapy. The polypeptides are also used for identifying compounds
CC modulating B-cell/T-cell mediated immune response with can in turn be
CC used for treating cancer, its related diseases and also for inhibiting
CC viral diseases by preventing viral infection.
XX
SQ Sequence 33 BP; 6 A; 10 C; 12 G; 3 T; 2 other;

Query Match 86.8%; Score 33; DB 21; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCGCCATGGCGCAGGTSCAGCTGCAGSAG 33
Db 1 CAGCCGCCATGGCGCAGGTSCAGCTGCAGSAG 33

RESULT 2

AAK99182
ID AAK99182 standard; DNA; 32 BP.

XX AAK99182;

XX 12-JUN-2002 (first entry)

XX 32-mer oligonucleotide #7 related to the invention.

XX Mouse monoclonal antibody; murine; surface antigen pres1 epitope;
KW hepatitis B virus; PCR; primer; ss.

XX Unidentified.

PN KR99008647-A.

PD 05-FEB-1999.

PF 02-JUL-1997; 97KR-0030694.

PR 02-JUL-1997; 97KR-0030694.

XX (KORE-) KOREA RES INST CHEM TECHNOLOGY.

XX Hong HJ, Ryoo CJ;

XX WPI; 2000-168375/15.

XX Changeable region of mouse monoclonal antibody recognizing surface
PT antigen pres1 epitope of hepatitis B virus and gene -

XX Disclosure; Page 8; 14pp; Korean.

XX The invention relates to a changeable region of mouse monoclonal antibody
CC recognising surface antigen pres1 epitope of hepatitis B virus and gene.
CC This polynucleotide sequence relates to a 32-mer oligonucleotide of the
CC invention.

XX Sequence 32 BP; 7 A; 6 C; 10 G; 6 T; 3 other;

Query Match 60.5%; Score 23; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGTSCAGTGCAGSAGTCWGG 38

Db 10 CAGGTSCAGTGCAGSAGTCWGG 32

RESULT 3

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 29.6585 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-11

Perfect score: 38
Sequence: 1 cagccgcatgagcaggtscagctcgagagtcwag 38

Scoring table: OLIGO_NUC
Gapco 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications_NA:*

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7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	42.1	1332	10	US-09-929-060-4
2	16	42.1	1515	10	US-09-929-060-5
3	14	36.8	22	10	US-09-253-794-43
4	14	36.8	22	10	US-09-742-693-13
5	14	36.8	22	10	US-09-742-693-19
6	14	36.8	22	10	US-09-217-2688-10
7	14	36.8	22	10	US-09-910-059-6
8	14	36.8	45	9	US-09-293-854-20
9	14	36.8	45	10	US-09-893-615-68
10	14	36.8	45	10	US-09-893-615-69
11	14	36.8	45	10	US-09-893-615-70
12	14	36.8	45	10	US-09-893-615-71
13	14	36.8	45	10	US-09-893-615-72
14	14	36.8	50	10	US-09-874-547-4
15	14	36.8	50	10	US-09-874-547-5
16	14	36.8	50	10	US-09-874-547-6
17	14	36.8	50	10	US-09-874-547-7
18	14	36.8	50	10	US-09-874-547-9
19	14	36.8	50	10	US-09-874-547-11

20	14	36.8	50	10	US-09-874-547-12	Sequence 12, Appl
21	14	36.8	50	10	US-09-874-547-13	Sequence 13, Appl
22	14	36.8	51	10	US-09-874-547-8	Sequence 8, Appl
23	14	36.8	51	10	US-09-874-547-10	Sequence 10, Appl
24	14	36.8	52	10	US-09-874-547-46	Sequence 46, Appl
25	14	36.8	52	10	US-09-874-547-47	Sequence 47, Appl
26	14	36.8	52	10	US-09-874-547-57	Sequence 57, Appl
27	14	36.8	52	10	US-09-978-752-1	Sequence 1, Appl
28	14	36.8	53	9	US-09-968-561A-343	Sequence 343, App
29	14	36.8	53	10	US-09-874-547-347	Sequence 347, App
30	14	36.8	53	10	US-09-874-547-40	Sequence 37, Appl
31	14	36.8	53	10	US-09-874-547-41	Sequence 40, Appl
32	14	36.8	53	10	US-09-874-547-43	Sequence 41, Appl
33	14	36.8	53	10	US-09-874-547-44	Sequence 43, Appl
34	14	36.8	53	10	US-09-874-547-50	Sequence 50, Appl
35	14	36.8	53	10	US-09-874-547-53	Sequence 53, Appl
36	14	36.8	53	10	US-09-874-547-55	Sequence 55, Appl
37	14	36.8	53	10	US-09-874-547-58	Sequence 58, Appl
38	14	36.8	53	10	US-09-874-547-59	Sequence 59, Appl
39	14	36.8	53	10	US-09-192-854-205	Sequence 205, App
40	14	36.8	53	10	US-09-192-854-209	Sequence 209, App
41	14	36.8	54	10	US-09-874-547-45	Sequence 45, Appl
42	14	36.8	54	10	US-09-874-547-49	Sequence 49, Appl
43	14	36.8	54	10	US-09-874-547-52	Sequence 52, Appl
44	14	36.8	54	10	US-09-874-547-54	Sequence 54, Appl
45	14	36.8	55	10	US-09-874-547-35	Sequence 35, Appl
46	14	36.8	55	10	US-09-874-547-36	Sequence 36, Appl
47	14	36.8	55	10	US-09-874-547-38	Sequence 38, Appl
48	14	36.8	55	10	US-09-874-547-39	Sequence 39, Appl
49	14	36.8	55	10	US-09-874-547-42	Sequence 42, Appl
50	14	36.8	55	10	US-09-874-547-48	Sequence 48, Appl
51	14	36.8	55	10	US-09-874-547-51	Sequence 51, Appl
52	14	36.8	55	10	US-09-874-547-55	Sequence 55, Appl
53	14	36.8	56	9	US-09-144-886-36	Sequence 36, Appl
54	14	36.8	56	9	US-09-144-886-37	Sequence 37, Appl
55	14	36.8	56	9	US-09-144-886-38	Sequence 38, Appl
56	14	36.8	56	9	US-09-144-886-39	Sequence 39, Appl
57	14	36.8	56	9	US-09-144-886-40	Sequence 40, Appl
58	14	36.8	56	9	US-09-144-886-41	Sequence 41, Appl
59	14	36.8	56	9	US-09-144-886-42	Sequence 42, Appl
60	14	36.8	56	9	US-09-144-886-43	Sequence 43, Appl
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65	14	36.8	56	10	US-09-988-899-46	Sequence 46, Appl
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67	14	36.8	56	10	US-09-988-899-48	Sequence 48, Appl
68	14	36.8	56	10	US-09-988-899-49	Sequence 49, Appl
69	14	36.8	56	10	US-09-988-899-50	Sequence 50, Appl
70	14	36.8	56	10	US-09-910-120-60	Sequence 60, Appl
71	14	36.8	56	10	US-09-910-120-61	Sequence 61, Appl
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75	14	36.8	56	10	US-09-910-120-65	Sequence 65, Appl
76	14	36.8	56	10	US-09-822-698A-39	Sequence 39, Appl
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92	14	36.8	933	12	US-10-052-798-8	Sequence 8, Appl

Sequence 7, Appli
Sequence 1988, Ap
Sequence 85, Appl
Sequence 1682, Ap
Sequence 36, Appl
Sequence 13, Appl
Sequence 2, Appli
Sequence 4569, Ap

93 14 36.8 939 12 US-10-052-798-7
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99 13 34.2 76 10 US-09-817-861-2
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ALIGNMENTS

RESULT 1
US-09-929-060-4
; Sequence 4, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1332

; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1329)
US-09-929-060-4

Query Match 42.1%; Score 16; DB 10; Length 1332;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGCCATGGCGCAGGT 20
Db 837 CGGCCATGGCGCAGGT 852

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; Sequence 5, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

Query Match 42.1%; Score 16; DB 10; Length 1515;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGCCATGGCGCAGGT 20
Db 1020 CGGCCATGGCGCAGGT 1035

RESULT 3

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; Sequence 43, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-253-794-43

Query Match 36.8%; Score 14; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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(without alignments)
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Title: US-09-424-705B-11

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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- Issued Parent NA:*
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 - 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	16	42.1	2363	2	US-08-609-426A-7	Sequence 7, Appl1
7	16	42.1	2379	2	US-08-374-652C-1	Sequence 1, Appl1
8	15	39.5	703	4	US-08-998-416-671	Sequence 671, App
9	15	39.5	1173	2	US-08-614-156B-4	Sequence 4, Appl1
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13	14	36.8	22	1	US-08-487-312-3	Sequence 3, Appl1
14	14	36.8	22	1	US-08-315-573-3	Sequence 3, Appl1
15	14	36.8	22	1	US-08-388-672A-4	Sequence 4, Appl1
16	14	36.8	22	1	US-08-480-434-1	Sequence 1, Appl1
17	14	36.8	22	1	US-08-480-434-83	Sequence 83, Appl1
18	14	36.8	22	1	US-08-657-012-3	Sequence 3, Appl1
19	14	36.8	22	1	US-07-934-373C-9	Sequence 9, Appl1
20	14	36.8	22	2	US-08-273-146-16	Sequence 16, Appl1
21	14	36.8	22	2	US-08-652-558-14	Sequence 14, Appl1
22	14	36.8	22	2	US-08-650-262-6	Sequence 6, Appl1
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61	14	36.8	45	2	US-08-814-806-20	Sequence 20, Appl1
62	14	36.8	45	4	US-09-813-781-3	Sequence 3, Appl1
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68	14	36.8	54	1	US-08-173-510B-37	Sequence 37, Appl1
69	14	36.8	54	1	US-08-173-510B-44	Sequence 44, Appl1
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71	14	36.8	54	1	US-08-458-218-44	Sequence 44, Appl1
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73	14	36.8	54	2	US-08-450-497-44	Sequence 44, Appl1
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75	14	36.8	56	1	US-08-211-202-25	Sequence 25, Appl1
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77	14	36.8	56	1	US-08-211-202-54	Sequence 54, Appl1
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79	14	36.8	56	1	US-08-211-202-56	Sequence 56, Appl1
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ALIGNMENTS

RESULT 1
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

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Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGGCCATGGCGCAGGT 20
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Db 837 CGGCCATGGCGCAGGT 852

RESULT 2
US-09-543-744-4
; Sequence 4, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-543-744-4

Query Match 42.1%; Score 16; DB 4; Length 1332;

Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 837 CGGCCATGGCGCAGGT 852

RESULT 3
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; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Aspergillus niger
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; NAME/KEY: sig_peptide
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; LOCATION: (157)..(183)
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US-09-155-855-5

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Best Local Similarity 100.0%; Pred. No. 5.2;
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RESULT 4
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855